

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGT**CATG**GCGTCCCGTCTCGGAGAC
TGCAGACTAAACCAGTCATTACTTGTTC AAGAGCGTTCTGCTAATCTACACTTTTATTTTC
TGGATCACTGGCGTTATCCTTCTTGCAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTGGTCGAACTGGTCGCTGCCATCGTAGG
ATTTGTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
TGTTGTGGTGTCACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTTCCCTTTGGAGTTGCTTGCTTCCAAGTATTGGAATCTTCTCGCCTACTGCCWCCTCTCG
TGCCATAACAAATAACCAGTATGAGATAGT**TAA**CCCAATGTATCTGTGGGCCTATTCCCTCT
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG
ACAACACTACTTACTGATAGACCAAAAACTACACCAAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTATGTTAGATCG
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FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGVSLNENYFSLLEKATNVPF
VLIATGTVIILLGTGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

Important features of the protein:**Signal peptide:**

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACGCGTCCGGCGCGCTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTACAAA
 GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGAGGTAGAGAAAGTCAGT
 GCCACAGCCCCACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
 TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
 GCCGGGTAGGCTCTGGAAGGGCCCGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGGGT
 GTTCCCTCTTTGCGGGGTCTCTACCAGAAAGAGGTTCTTGGGGGTGCGCCCTTCTGAGGAGGCT
 GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCTGTAGTTGATAATGTTG
 GGAATAAGCTCTGCAACTTTCTTTGGCATTCAAGTTGTTAAAAACAAATAGGATGCAAATTC
 TCAACTCCAGGTTATGAAAACAGTACTTGGAAAACGAAAACACCTAAATGATCGTCTTTG
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
 CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
 CCGAGATGACAGTGAACAGATGACAGTGTGACACCAACAGCAACAGGCCGAGAACAGTG
 CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCTGTTTCGGCCACCAAGGAGGGGC
 CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTGGACACACT
 GGCAGTAATACGGACTCTTGTAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
 GAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
 TGATAAGATTTGATGTTTTTGCTTGCTGTCTACTTTGTCTGGAATGTCTAAATGTTTC
 TGTAGCAGAAAACAGATAAAGCTATGATCTTTATTAGAG

FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEIHAFGLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNV DGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTAGCCCCATTTGGCC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTAACGGACTG
CAAGATGGAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCTGGGGCATGCAAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTCCCCCTTCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCTTGAGCCTTACGCTGGCCACTGTCAAC
GCCCCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTCCGCTACCATGGGCTGTCC
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA
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AAAAAAAAAAAA

FIGURE 6

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<subunit 1 of 1, 231 aa, 1 stop
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<NX(S/T): 0
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GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAAMWALQTVEKER
GLGGEVFGSHQGPDPYRQLREKDPKYSALRQNFERYHGLSSLCNLGCVLSNGLCLAGLALEIRSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTCAGATTTTAAAGCCATTCTGCAGTGAATTTTCATGAACTAGCAAGAGGACACCATCTT
 CTTGTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGAAAAATGCTCTTTTGGGT
 GCTAGGCCCTCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAG
 ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAAACTTGGCAGCC
 AGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC
 AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG
 AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGAGAAAGGTCTCTGGGGT
 CTGATCAATAATGCTGGTGTTCCCGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGA
 CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTIONCATCAGTGTGACACTAAATATGCTTC
 CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTGCGCTTGCA
 ATCGTTGGAGGGGGCTATACCTCCATCCAAATATGCAGTGAAGGTTTCAATGACAGCTTAAG
 ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA
 ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAACCTGCCATTGGGAGCAGCTGTCTCCA
 GACATCAAAACAACAATATGGAGAAGGTTACATTGAAAAAAGTCTAGACAAAAGTAAAGGCAA
 TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
 GTCTCTTCCCTAAGACTCATTATGCCGCTGAAAAAGATGCCAAAATTTTCTGGATACCTCTG
 TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
 TCCCAAGGCAGTGTGACTCAGCTAACACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT
 TTCAAGAACACATCTCCTTTTCAACCCATTCCTTATCTGCTCCAACCTGGACTCATTAGA
 TCGTGCTTATTTGGATTGCAAAAGGGAGTCCACCATCGCTGGTGGTATCCAGGGTCCCTG
 CCAAGTTTTCTTTGAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTGCCCTGT
 ATTTAGGCTTTGCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAATG
 ATCTTACCGTGGCTGCCCCATGCTTATGGTCCCAGCATTACAGTAACTTGTGAATGTT
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 AAAAAAAAAAAAAAAAAA

FIGURE 8

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LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCEIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

CGCGGCTGTGTACGGCGCTGCG**ATG**GCTGCCGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
CCTCTCAGTCGGAACTTCTTGACCGCGCCATGTGGCGCGGCCCTTGGGCGCTCGCCACCACCT
GTAGTCAATGATACCCACGCGCGCGCGCGCTCATCGGAGCTTCATCTCGTGACGCTGAG
CTTTTGGCGAGAGCGTATGACAAACAGCAAGAGTTGGCGCGCGCGCTCGTGCTGGAGGAAATGG
AGCAACTCTGAGAGTTGACCGGGAATATGATTCTCTTCCGCTTTCTGCTTTTCTGT
GGACTCCTCTTCTACATCAACTTGGCTGACATTGGAAAGCTCTGGCTTTCAGGCTAGAGGA
AGAGCAGGAAGTGAAGGCCAGAAATCTGTGGTTTAAACACGAAATCCACCCTGCTTACAG
CTCTCTCAGAAAGGCGACACCGACCTTGAGAACTTACCTGAGATTTCGTCAAGAACACACA
AGACACATCCAGCGGGACCACTCACTGCAGATTAGACCCCAAGCCAAAGCCTGAAGGA
TGGGACCCAGGAGGAGGCCACAAAAGGCCAAGAGCCCTCTGGATCCCCGCCGCGGAAGGAG
ATCCGACAGGACAGTCACTAGCTGAGGGGAGCGGTATCGACCTTGAGACGGGACCGAG
CTCCTCTCAAGAAGAGAGCAAGTGGCCACCAAGCTCCCTCGCACCGGCCAGGACACAGGG
CACACAGTGCATCTGAATCTGCCAGAAGGGCGTGATTGACGTTTCTCTGCATGATCGATGA
AAGGATACCGCAAGTTTGCATGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCTTCAGT
GAGTGGTTTGGCTCGGTTCTCACACTGATCGACGCGCTGGACACATGTGGATCTTGGGTTCT
GAGGAAAGAAATTTGAGAAGCCAGGAAGTGGGTCTCGAAGAGCTTACACTTTGAAAAGGACG
TGGACGTCACACCTGTTTGAAGACAGATCGCATCTGTTGGGGGGCTCTGATGTCCTACAC
CTGTCTGGGACAGCCTTCTTCTGAGGAAAGCTGAGAAATTTGAAATCGGTAATGCTGCTG
CTTCAGAACCACCTCAAGATTCTTACTCGGATGTGAACCTCGGTACTGGAGTTGCCACC
CGCCACGGTGGACTCCGACAGCACTGTGGCCAGGTGACCAAGCTTCAGCTGGAGTTCCGG
GAGCTCTCCGCTCTCACAGGGGATAAGAAGTTTACAGGAGCATGGGAAGGTGACACACAGA
CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCAAGTAC
GCTCTTCCACCCCACTGGGCTATTACGCTGGGCGCCAGGCGCCAGCTACTATGAGTATG
CTGTCTGAAGCACTGGATCTCAGGCGGGGAAGCAGAGACACAGCTGCTGGAAGACTACGTGGA
AGCCATCGAGGGTGTCTCAGAAGCCACTGCTCGGCCAGCTCCGAGCCGATAGCTACCTTTGT
TGGGGAGAGTCTGCCACGGCCGCTTCAGTGCCCAAGATGACACACTGGTGTGCTTCTGCCA
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GCTCATGGAGACTTGTTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCAGATCG
TGCACCTCAACCTTTACCCCCAGCGGGCGCTCGGAGCTGGAGGTCAGGCCAGACAGG
CACAACTGCTCGGCCAGACAGACCTGGAGACGCTGTTTACTGTATCCCGCTCAGAGGGG
CCGCAAAATACAGGACTGGGCTGGGAGATTCTCGACAGCTTACGCGGATTACACAGGGTCC
CCTCGGGTGGCTATTCTTCATCAACAATGTCCAGGATCCTCAGAAGCCCGAGCTTGGGAC
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CCCCAACTGCTCAGCTGGACGCTACGTGTTCACACCGAAGCCACCTCTGCTATCT
GGACCTCTGCC**TAGG**GTGGAATGGCTGTGTGTGGGGACTTCGGGTGGGCAGAGCACTTG
CTGGGTCTGTGCTTTTCAAAGGGCCCACTAGACACCGCAACCCGCAAGTGGCCAGGCT
CTGAATCGGCTCTGGGCTCCTCTCTGCTCTGCTTTAATCAGGACCCGTGAGGACAAAGTGA
GGCCGTCAGTCTTGGTGTGATGGCGGTTGGGCTGGGCGCTGAGGCTCCGGCTGCTTCTC
CAGAAGACAGAAATCAGTACATCAGACTTGTGAAGCTTGAGGAGTCTGTGTGGGCGACCA
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CTGGCCCGCCCGCAGGGGCTTGGAGGGCTGGAGCGGAAGTCCGTCTAGCTCAGGGCCCTC
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FIGURE 10

```
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SKSWRRRSCWRKWKQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTTQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTLEPSRRAEVPTKPPLPARTQGTTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRFSSEWFGGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFESTITIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSDSTVAEVTISIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVTILGARADSYEYLLKQWIOGGKQETQLEDYVEAIEGVRT
HLLRHSEPSKLTfVGEIAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQGRRDVEVKPADRNLLRPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD
AYVENTEAHPLPIWTPA
```

Important features of the protein:**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC
 CGCCTCTCCGCACG**ATGTT**CCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC
 AGGTCGGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTCTGTGGC
 CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
 CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCCCCCCGTGCTGCCCCCAGAG
 CCGCCCCCTGAGCACTGGGAAGAAGACGCATCTGGGGCCCCACCGCTGGCAGTGCTGGT
 GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGA
 GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC
 CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT
 GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTTCTGAGGCTGGGC
 CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCCTACAAGACCTATGTGCGCGGC
 ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG
 CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAAGGAGCTGGGCTCCAGCTTTTCC
 GCCCCTCGGGAATCACAACTGGGTACAAGACATTTCGCCACCTGCATGACCCAGCCTGGCGG
 AAGAGGGACCCAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG
 AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC
 CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCTGGTGCACATTC
 AGC**TGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA
 CAAGGCCTCAGGTCGTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
 AGCTACGCAATTGCAGCCACCCGGCCGCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG
 GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGCTCTGTCCG
 GGACCCCCCTGCCTTCTGTCTACCCCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGG
 TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCC
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FIGURE 12

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RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHVDVLLPLNEELDYGFEAGPFHVA
SPELHPLYHYKTYVGGIILLSSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS
```

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATGTTTGCCTATCCACCTCCCCAAGCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCT
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCTTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT
GGGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGG
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC
CCTGTTCATTAAGAAATGTTCCCTTCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGT
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FIGURE 14

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

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PRGEGEKVGDG

Important features:**Signal peptide:**

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG
 GAGCATGTCGCCGCCGCCGGGAAGGCCCGTCTCCGGCCGCCATAAGGCTCCGGTCCGCCGTGG
 GCCCGCCGCCGCTCTCTGCCGCCGGGCTCCGGGCCGCCGCTAGGCCAGTGCGCCGCCCG
 CTCGCCCCGAGGCCCCCGGCCCGCAGC**ATG**GAGCCACCCGGACGCCGGCGGGGCCGCCGCA
 GCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGGCGGGCGG
 GCGGGCGGCCCGCGGCTGCCGCCGGCTGCAAGCACGATGGGCGGCCGCCCGAGGGGCTGGC
 AGGGCGGGCGGCCGCCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACCTCGCGCAGGTCCT
 GCCCCAGATACTCTGCCCAACCCGACGGTACCCCTGATTCTGAGTAACAATAAGATATCCG
 AGCTGAAGAATGGCTCATTTTCTGGGTTAAGTCTCCTTGAAAGATTGGACCTCCGAAACAAT
 CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTGATCTCTAAAAAGATTGGATCT
 GACAACAATCGAATAGGATGTCTGAATGCAGACATATTTTCGAGGACTCACCATCTGGTTC
 GGCTAAACCTTTTCGGGGAATTTGTTTTCTTCATTATCTCAAGGAACCTTTTGATTATCTTGGC
 TCATTACGGTCTTTGGAAATCCAGACTGAGTATCTTTTGTGTGACTGTAACATACTGTGGAT
 GCATCGCTGGGTAAGGAGAAGAACATCACGGTACGGGATACCAGGTGTGTTTATCCTAAGT
 CACTGCAGGCCCAACAGTACAGGGCGTGAAGCAGGAGCTGTTGACATGCGACCCCTCCGCTT
 GAATTGCCGTCTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTTGAAGGAGACGCCCT
 TCCTTTCCAGTGATGGCTTCATATATTGATCAGGACATGCAAGTGTGTTGGTATCAGGATG
 GGAGAATTGTGAACCGATGAATCGCAAGGTATTTTGTGTTAAAGAAACATGATTCACAAC
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 GAGCTCACGTTTATTCACATATTCACCCAATATTGCTCTGGAAGCTTATGTATCATCAAGTCT
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 ACTTTTCGGAATTTGGAGGCGGGATCCAGAGGGAACCTGGATAAGCAGTGAAGCTTTAAGT
 GCAATGTTTCAAATACATTTTTCGAGTCTGGCAGCTAAAGGTATGTTACATTCTGCAATCATTT
 AAGACTATTTACAGT**TAA**AATTAGAATGCTCCAAATGTCTGCTTCGCAAAATAACCTTATTTA
 AAGATTTTTTTTTTTCAGGAAGATAGGTATTATGCTTTTGGCTACTGTTTAAAGAAAACATA
 ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTGGCTTTGATTCCTTT
 CTTACATAAAAAATATCAGAAATACATTTTATAACTGCAGTGGTATAAATGCAAAATATACT
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 GATTTTAAGCAATAAAGATTTTTCATGGGCCCTTAAAGTATCATGAGCCTTTGGCAGCTGC
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 ATCAAAATTTTGGCAGAAAACCAAAATATGTATATATCTTTTTTAAAAAAGTATTTCA
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 TACTTTTATTTCTGTCTTGTCCCTCAATAATACACAACAATATCCAGCATCTTTAATGGC
 TGCATAATACTGATCCAAAGGTTAGTGTCTGTTTGTAGTGTGAGCATTCAATAAATA
 TTGAATGAATGAACGAAAAAAAAAAAAAAAAA

FIGURE 16

MEPPGRRRRGRAQPPLLLPLSLLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
VVCSSLELAQVLPDPTLPNRTVTILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
FWGLSSLKRLDLTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLFQTF
EYLLCDCNILLWMHRWVKEKNITVRDTRCVPKSLQAQPVTVGVKQELLTCDPPELPSFYMTF
SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT
ISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWERTLAGITA
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNLN
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLA
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
VFQKVAASDRITGLSDYGRDPEGNLDKQLSFKCNVSNFTFSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
384-390, 403-409, 554-560

FIGURE 17

GCCTGGGG**ATG**CTAGGAGCTCGAAGGTGGTGTGGGCCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGCCCGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCCAAATTCGGAAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAA
TCAT**GCA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTGGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGAGGGGAGAGACGCTCCTGATCGTCGAATCC

FIGURE 18

MSRSSKVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

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FIGURE 19

CTGTGCTCTTTTGCTTCAGCCGCAGTGCCTACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTCT
CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGTCTAAGACC
GCTGCCATGCCAGTGACGGTAACCCGCACACCATCACAAACCACCAGACGTCACTCTTCGGG
CCTGGGGTFCCCCATGATCGTGGGGTCCCCTCGGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC
CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAG
GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGCTTCTGCTTCTCCGTGACCCTGATCA
TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC
ATCACCTTCGCTGCTATCGGGCCCTCTTCTGCTCTCGGCCCTCCATCATCTACCCACCAC
CTATGTCCAGTTCTCTGTCCACGGCCGTTGCGGGGACACGCCATCGCGCCCACTTCTTCT
CCTGTCACTGCGTGTGTGGCTTACCGCATCCGAAGTGGCTTGGACCGGGCCGGCCCTGGCGAG
ATCACTGGCTATATGGCCACCCTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCTTGCTGTG
CATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT
GCGTGGCGGTGTACGCCATCTGCTTCATCTAGCGGCCATCGCCATCCTGCTGAACCTGGGG
GAGTGCACCAACGTGCTACCCATCCCCCTCCCGAGCTTCTGTGCGGGCTGGCCTTGCTGTG
TGTCTCTCTATGCCACCGCCCTTGTTCTCTGGCCCTCTACCAGTTGCATGAGAAGTATG
GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGACGCCATGCCCTACTACGTGTGT
GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC
TGACCTGGTGACTCTGCCACCTGGTTTTTGTCAAGGTCTAAGACTCTCCCAAGAGGCTCC
CGTTCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCC
TCGGCCTTTTCTCTGTTTTCTCTTCTGTCTCCCTCCCTCCCACTTTTCTTTCTTCTTC
CAATTCCTTGACTCTAAACAGTTCTTGGATGCATCTTTTCCCTTCCCTTCTTCTCTGTCTG
TCTCTCTCTGTGTGTTTTGTTGCCACATCGTCTTTTACCCTGAGCTGTTTCTCTTTTT
CTTTTCTTFTTTTTTTTTTTTTTTTAAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG
TGCAGTGGTGCGATCTCAGCTCACTGCAACCCCCGCCTCCTGGGTTCAGCGATTCTCTCTC
CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTTT
TTCACACTCTTCTTTTTTCTCATCTCTTTTCTGGGTGCTCTGTCGGCTTCTTATCTGCCTGT
TTTGCAAGCACCTTCTCCTGTGCTCTTGGGAGCCCTGAGACTTCTTCTCTCTTGCCTCCA
CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGCAGCCGTCATGCCACAGCCCC
CCAAGGGGCCCAATTGCCAAGCATGCTCTGCCACCCCTCGCTGTGCTTAGTCACTGTGTAC
GTGTGTGTGTGTGTGTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT
CCCAGTGGAGGAAGGTGTGCACTGTACTTCCCTTTAAATTAAAAAACATATATATATATAT
ATTTGGAGGTCACTAATTTCCAATGGGCGGGAGGCATTAAGCACCAGCCCTGGGTCCCTAGG
CCCCCTGCTGCCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTTCAGGCTTACAGAACAC
CCACTGCTTACAGCCCATCTTAAAGGAAGCAGGGCTGGATGCCTTTCATCCCACTATCTCT
CTGTGGTATGAAAAAG

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTTTTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLIIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPALWECVAVYAICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 21

GAAGCTGCCACCATGCCAGCTAATTTTGTATTTTTAGTAGAGACGGGGTTTACCATGTTGGCCAGGCTGGTC
 TTGAAGTCTGCTGACCTCATGATCCGCTCACCTCGCCCTCCCAAAGTCTGGGATTCAGGCATGAGCCATGAGCC
 CTGGCCAGCCTATGCATTTTTTAAAGAAATTTCTCTATTAGGTGCTGTGCTAAACATTGGGCATCAGCTGACCA
 AAACAGACATGAATTCCTCCAAAGAGCCAAAGACAGTGGAGGAGACCAACAAGAAACAGGAATGCAAAAGAGACCA
 TTATTACTCATATTGACTAAGGGTACAAATGGGGTACGTTGATGGAGAGTGTATTGTTAAGAGACTACAGAGGG
 AGGACAGACTACCAGAGGGGGGGCCAGGAAAGCTCCTCTGACGAGGTGGTATTTACGCCCAAATCGGAAGATGA
 GAAAGAGCTAGCCAGCCATCAGAAATAGTCCAGAAAGAGATGGGGAGCACTACACTACACTTGGCCTGAGAA
 AATAGCATGGATTTGGAGGAGCTGGGGAAACACCACTCTCGCCGACCTGGCCAGGAGGCATTGAGGCTTGAGA
 AAGGGCAATTGGCAGTAGCAGTAGAAAGGACAGGGTAGGAGCAGGGACTTTGCAGGTGGAATCATTAGGCTTTATC
 AACAGATATGGGCAGCAAAGCCAGGGGAGAAATTGATGGTAATGCTGAGGTTTGGAGCCAGGCTAGATGGGACAG
 TGGTGGGTGATGCAAAAGGAAGAGGTGAGGAAGCAGGGCCAGACGTTGGGGAGAAAGTGTGGGGGTTTGGTTTCCA
 TCTTGCCGAGTCTGCCGAATGTGGATGGGAAGACCAAGAGGAGGAGCAAGGGGAGAGGGGAAAGGGAATCTTAA
 AGAAGTCTGGATGCCACACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAT
 TTCTCGCCCTGCCCTCATCTCTCTGGGTGCTGGGAAAGTGGAGGATAGCTGAAGTTTGTCTCTCGGGGCTG
 TCTGAATCTCCATTGCTTTCTGGGAGGACATAATTACCTGTCTTACCTCTTATCATCTTACATTTCCCTGTAG
 CCAGTGGGACATATGTGGTGTCTCTCTAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 GGGGAGGTCATTGCTGTGAGAGGGGCACTGACTTTCTAATGGTGTATCCCAAGGTGAATGTTGGAGACACAGCT
 GCGATGCTGCCCAAGTCCCGGCGAGGCTTAACTATCCAGGAGATCGCTGGCCGTGCCAGGCTCTCCCTGCATGGT
 ATGCAGCCCTCCATGTTTCTGGGCACTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 GTGAGTACATGCTGGGCTCTCCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 ACATGATCTCTAATCATGCCACCTTCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 TCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 GCGAGTGGCTCACTCATGATGGTGAAGGGCTGGAGCAAGCCGAGTGACTCACCTGCTGCTGCTGGAATCAGGCT
 TTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 TCCGGAAGCCAAAGTCCGAGCATGGTCTTCTGGTGGATGGCGAGGACTCCATGATGATGATGATGATGATGATGATGAT
 TTGCTGGGGGAATGGACACAGACATGGCTGGGCACTGCCCTGGGGCCGCACTCTCCAGAGCTGTTCACGGGCC
 ACCGTTCTCTCCGCGCTGTGCCAGGAGGCTCCGTTGGAGCTTGAGAGGAGTGTCTCACAGACCGTGTCTCCACAGCA
 CCTGTGCTCTAGTCTGTGCAGCTTGGAGGATGGTGTGTGGGCTCCCGGCGCGGCTGGCTCCAGCTGCTGTGG
 GCGATGAGTGTCTCTGCGCAACTGCCGCCAGCCGCGGAAAGTGCCTTCCGAGGCTGGGCGCACCTGGAGGGCC
 AGGACTCACTCTACAACCTGCCCTCTCACAGATCTGCTCTTCCCGCGGAGGAGGAGCCAGCCCTGCAAGG
 ACTGCCAGCCACTCTGCCACCACTAACCGGCGAGTGGGAACGCGAGCGGCAAGGCTCTGACCTTGGCTCTCTCTG
 GGTGGTGTCTCTTAGATGAGGATGAGGCAAGCCAGAGGAACAGTGAACCACTCATGCTGGCAGTGGCATGCA
 TCCCGCGGCTGCTGCCAGGGGAGAGGCTCTGTGCCCAAGTGTGGGCTCAAGGCTCCAGCAGAGCTCCACAGCC
 TAGAGGCTCTCTGGGAGCGCTGCTCTCTCGTTGTGTGTTTGCATGAAAGTGTGAGAGGAGGAGGAGGCTG
 GGTGGGGGCGCATGTCTGCCCCCACTCCCGGGGCTTGGCGGGGCTTGGCGGGGCTCTTGGGCGCATGGCTACA
 GCTGTGGCAGACAGTATGTTATGTTCTTAAATGCCACACACATTTCTCTCTCGGATAATGTGAACCACTA
 AGGGGCTGTGACTGGGCTGTGTGAGGTTGGGTTGGGAGGGGGCCAGCAACCCGCCCTCTCTCTCTCTCTCTCTCTCT
 TCTTCTCTGCTTTTCTCTCTCTCTCCAGTCCATGTGCACTGCTTGATAGAAATCACCCCACTTGGAGGGGCTGG
 CTCTCTGCCCTCCCGGAGCTATGGGTTGAGCGTCTCTCAAGGGCCCTTGCAGGCTGGGCTCGTCTGTGCTTCT
 ATTCACTCTCCATCGTCTCTAAATCTCTCTCTTTTTTCTAAAGACAGAAAGGTTGCTGCTGTTTTTGTCTGCT
 GGATCTCTCTCTCTGGAGGCTTTGGAATGATGAAAGCATGTAACCTTCCACCTTTTCTCTGGCCCTCTAATGG
 GGCTGGGCGCTTTCCCAACCTCTCTAGGATGTGCGGGCAGTGTGCTGGCGCTCACAGCCAGCCGGCTGCGCC
 ATTACGCGAGAGCTCTGAGCGGAGGTGGAAGAAAGGATGGCTCTGGTGTCCACAGAGCTGGGACTTATGTT
 CTCTAGAGAGGCTACAGTACAGGAGGCGCCAGGGTGGCGGGAGTTGTGACGTGATGCTGTGAGAGGAGGAGAT
 GTGCGAGTGAAGTACAGTATGAGGAGTGTCTCTCTTGGGAGGAAAGAGGATGAGCGCTTCTGTCTGAAT
 GAGAGGCGAGGCTACAGTACAGGCGCCCGGCCAGCGAGGTTGTTAATGCCCACTGTGGAGGCTCTGCGAG
 CTCTGCAATCCAAGTCACTGGATGTACGTTTATGTTGTGGGAGGGTGGTGGCTTTAGAAATTAAGGCG
 TTTGAGGCTTTGGCAGTGAAGGCGCAAGGTGAAGACGAGGCAACCGGCAACGATCTATATTAAGT
 GGCTCATTAGGTGTTTATTTTGTCTATTTAAGATTTGTTTATTAATAATATAAAAAATCTTTGTAATCTC
 TAAAA

1015715.123001

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKVMHDPNYCHPSTSLHLCS
 LAWSFTRLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALSAFSSY
 SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
 PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPDTLCSLCSLEDGLLGS PARLASQLLGDE
 LLLAKLPSPRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
 QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
 285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCT
GGCACCTCTGCTCAGTGCACATTGTACACTTAACCCATCTGTTTTCTCTAATGCACGA
CAGATTCCCTTCAGACAGACAACCTGTGATATTTTCAGTTCCTGATTGTAATACCTCCTAAG
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA
TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCTTTAAAAAAAACCAATACCAAAG
AAGCCTACA**ATG**CTTGGCCTTAGCCAAAATCTGTTGATTTCAACGTTGTTTTATTCACTTCT
ATCGGGGAGCCATGAAAAAGAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT
TTAAACAATGAAAAATAACCTATTCTTTGAAAAGTGAAGCAAACCTAAACTCAGATAAA
GAAAAATATAACCACTCAAATCTCAAGGCGAGTCATTCCCTCCTTTGAATCTACCCAACAA
CAGCCACGGAATAACAGATTTCTCCAGTAACATCAGCAGAGCATTCTTTGGGCAGTCTAA
AACCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTGTTTCTAAAGTGCCCT
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC
TGCTCTGTCTTCAGAAAACCTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATA
ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG
ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA
TCAAGAAAAACAACCTCTACAGCCTACCTTAAATTCACCAATAATTCAAAACCTCTTTCCAA
ATACGTCAGATCCCCAAAAAGAAAATAGAAATACAGGAATAGTATTGCGGGCCATTTAGGT
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGTGGAAGGAAAAC
GGATTCAATTTCCATCGCGACTTTATGACGACAGAAATGAACAGTTCTGCGATTAGACA
ATGCACCGGAACCTTATGATGTGAGTTTGGGAATCTAGCTACTACAATCCAACCTTTGAAT
GATTACGCCATGCCAGAAAGTGAAGAAAATGCAGTGATGGCATTCCCTATGGATGACATACC
TCCACTTCGTACTTCTGT**AG**AACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTATCTA
CATCCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGAT
TTTGTCAGGAGAATCATAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
CCAAAGGTTTTCTTTCTTACAATTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT
TGATTTTTAGTAGTATTTCTTAGTAGAAAATATTTGTGGAATCAGATAAAAATCAAAGATT
TCACCATACAGCCCTGCCTCATAACTAAATAATAAAAATTTATCCACCAAAAATTTCTAAA
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT
TTTCTTAAATGAAAATTGAAAGGGTGCTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG
GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC
TAGTACGTTATAATTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA
CAATGACTGCATTCAACGGGGCCATGGCAGGAAGCTGACCCACCCAGGAAAGTAATAGCT
TCTTTAAAGTCTTCAAAGGTTTTGGGAATTTAACTTGTCTTAATATATCTTAGGCTTCAA
TTATTGGGTGCCTTAAAACTCAATGAGAATCATGGT

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSSENF TWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLPNTSDPQKENRNTGIVFGAILGAIL
GVSLTLVGYLLCGKRKTD SFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNP TLNDSA
MPFESEENARDGIPMD DIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTTGCAGTCTGCAGCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
AGCCCGAAGATTCACT**ATG**TGTGAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG
AGGCGCGGCAAGACGTGGAGGCCCTCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
CTTAGGCCCTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTACAAAGTAC
TCATGCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA
AATTCCCTTCGTGGAGGAGAGCCTAACTTCTGCCTGTGACTGAGGAGGCTGACATTCGTGA
GGATGACAACATTGCAATCATTTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCTGCAG
CAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTGCTGGGGAACCTG
TATCTGATGGCCCTCAATACTCTATTGTTATGCTCCAAAAATCTGGTAGAGCTCTTTGG
CAAACTGGCGAGTGGCAGACTTATGCCTCAAACCTTATGTGTTGCGAAGAGACCTAGTTGCTG
TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTTATTACCAACTTTGCAATAACAGA
AAGTCTTCCGCCCTTCGTCGCAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA
ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAG**T**
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA
CATTAAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT
AAAAAAGGAAAAAAAAAAAAA**AA**CTACTAACCACCTGCAAGCTCTTGTCAAATTTAGTTTAAT
TGGCATTGCTTGTTTTTTGAACCTGAAATTACATGAGTTTCATTTTTCTTTCATTATAG
GGTTTAGATTCTGAAAGCAGATGAATATATCACCTAACATCCTGACAATAAATCCATCC
GTTGTTTTTTTTGTTGTTGTTTTTTCTTTTCTTTAAAGTAAGCTCTTTATTATCTTTATG
GTGGAGCAATTTTAAATTTGAAATATTTTAAATTTGTTTTGAACTTTTGTGTAATAATATA
TCAGATCTCAACATTGTTGGTTTCTTTTGTTTTTCATTTTGTAACCTTCTTGAAATTTAGA
AATTACATCTTTCAGATTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAAT
TTCATGAGACAGTCATGTTTTAACTAATGAGTGAATCTTCTTCACTACTATCTGTATTGTGG
AATGCACAAAATCTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATCTACAA
CCCTATAATAAATTTTAACTCTATACAAAAAAGAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVRTQILTGKELRVATQKEGSSGRCLTLGLGSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLGNCYLMPLNTSIVMPPKNLVELFGKLAGS
RYLPQTYVVREDLVAVEEIRDVSNLGIIFYQLCNNRKSFRLRRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGGAGGAGGAGGGCGGGCAGGCGCCAGCCAGCAGCCCCGGGACCAGCAGCGACTCTCT
 CTTCCAGCCCAGGTGCCCCCCACTCTCGCTCCATTCTGGCGGGAGCACCCAGTCTCTGTACGCC
 AAGGAACTGGTCTTGGGGGCACCAATGTTTTCTGGCGGCAGCCCCAGCCTCCTCATCTTCTG
 TTGCTGCTGCTGGGGTCTGTGCTCTGTACCGACGCCGCTCTGTGCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGGTAGTGGGAGGCCGAGGGCTCGTTCGGCCTCCTCCCCAGCCTCC
 CGCCACCTTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCAACCTGGGG
 GGCCCATCACCCCCACCAACTTCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGGCTCCTTGGCCTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA
 TCACCCGGCAGAAGCAGAAGGCCTCGGCCATTATACCATCGTCTTCCCCAAGAAGAAGTAC
 GTGGACCAGAGTGACCGGGCCGGGGGCCCGGGCCTTCAGTGAGGTCCCGACAGAGCCCC
 CGACAGCAGGCCCGAGGAAGCCCTGGATTCTCCCGGCAGCTCCAGGCCGACATCTTGGCCG
 CCACCGAGAACCTCAAGTCCCCCAGCAGGGCTGCATCGGGCGGTGGGACGAGCAGGAGTCA
 GTGGAGGGCAGGGGCGCAGCCAAAGAGGAGGAGGCGAGGAGGGGGACAGGAAAGTCCA
 GGGACATGGGGTCCAGTGGAGACACCAGAGGCGCAGGAGGAGCGTGTCTCAGGGGTCTCTG
 AGGGGGCTGTGGTGGCCGCTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTTAGCCAG
 GAAGCCCAGGGACCAGTGGGTCCCCCGAAAGGCCCTGTGCTTGCAGCAGTGTCCACCCAG
 TGTCTTAACAGTCTCTCCGGGCTGCCAGCCCTGACTGTTCGGGCCCCCAAGTGGTCACTCCCC
 GTGTATGAAAAGGCCTTACGCCCTGACTGCTTCTGACACTCCTCCTTGGCCTCCTGTGG
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCGGTCGCCCGGA
 GGAATCTTACCAAGTGCCATCATCTTCACCTCAGCAGCCCCAAAGGGCTACATCTTACAGC
 ACAGCTCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGCTGGGATTACAGCGGTGAGCCACCGTGCCCGGCCCAAACACTACTTTTTAAACA
 GCTACAGGGTAAAATCTTCAGCAGCCCACTCTGGAATAACTGCTCTTAATTTCTGAAGG
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCTC
 TCAAGCGCTCTCCAAGCACCCCGGGCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG
 GATCAGGTTGAATGAATGGAACCTCTCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTTGAGGGGACCTCCACCTTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG
 CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG
 TGTCACAATATTCTGTAGTCTCGACAGGGAGCCTGGGCTCCGTCCTGCTTTAGGGAGGCT
 CTGAGCAGGAGTCTCTCCCCACTCCCTCATCTGGGGCTCCCCAACCTCTGCACAGCTCT
 CCAAGGTCTGAGATATAATGCACACAGCAATAAACCTTTATTCCGGCTGAAAAA
 AAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPTNFDGIVDFFRQYVMLIAVVGSLAFLMFIVCAAVITRQKQKA
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPSCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPPESPCACSSVHPSV

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 29

[illegible]

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGFPLACLLALLCLSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGLGGQGQGNPGGLGT PWVHGYPGNSAGSFGM
NPQGAFPWQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQSGSSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSGSSSGSGSGNSGSGSRGDSGSESSW
GSSTGSSSSNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRRQGVSSNMREISKEGNRL
GGSGDNYRQGSSSWGSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDINKDQ
RSSRIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

ACCGGTCCTCTCGGGTCTCTATGTGCGGACTCTGCTACAGCAGGGCTCGAGCGCGCGCGGGAGTCTCACTCA
TGGCTGGCTGGTGGAGGTTCTCTCTTCTGCTACAGATGTGTCTTCTCGGAATATAACGGCAGATCTTCA
CTCTCTCTGCTGCGCTGCAACGGAGCTTGGTGTGTGCGAGGAGAGTGAGGGCAAGATGTTTCTTCTGAACAAGC
TGCTGTGATCTTGCTGTCTGGGCTGGCTTTTCAGATTCCACAGCTCTTGAGACATTTCTTTCTTGGAAAGGCT
GTCTCTCTATGTCTTGAAGTGGACACAGTACGCCAGAGCATGGTCTGGCAATGCCCTTGGTGGACGAGC
AGTCTGCTTACACATCTGCTCCCTCATATCGGAGAGCTCCGGAATCTGCTGCTTGTGGGTGTACGAGGATAGT
GACGAGTAGTGGGGCTTCATGAGAAATACCCAGCCACCATACACACGCTGGGAGCGACGCTTCCAGAGTAC
CGAGGGGCTCGAGGCACAGCTCGCCAGCGCTTTTCCACACACAGCGCCCTCTTGTGGCGGACCGCTAGAG
TCGTGGCAGAAAGAAATGGATCAAACTGTGTCAAACATATCAAGGTACACTGGTGGCAGATGTGTGTCGCGG
CAGAGCTACTCTTCCAAAGCAGCTGGTGACACAGGAGGAAGGAGGAGACCGACCGCTCAAGTGTGGAGATCT
TGTTTTCACGCTGTGCCCTCGAGGGCGCCAGCATATGGCTCTGGGGGGGAGTGTCTGCAAGGAAGAGCCCTG
GGGCTGTGGCGGCTGCTTTCAGAGAGACGCCCGGACAGCTCTGTGAGCATGTGAGAGAAATCTGCTGTGGGG
TTGCAACAGAGAAGAGCTGTGCTTGGCTGTGACGCAACATACAGACATGATCAGGAGGGAGGTGAAGACGAGC
TGAGTGCACACTCTCGAGCGCAGGCTCTGAACTGCTGCGCGGGGGAGCGGGGCTGTCTCCGCGCTCGAGC
GTGCTCTCTTGGCGCTGGGGCGCAGGGACCTGACGAGGAGATCTCCACAGAGATCTGGAACAGCTCTTAGGC
CAGCTGGGCGACAGCTCGGGGTGCGCGCACTTCTGTGCCACATCTGTAGCAGCATCTGCGAAAGTGTCTGTG
GTAGTTAGTCTTCTCTCTGTGACATCAAACTCTATCTTAGGCGCCCGGACAGCATGACAGCTGGAGAGAGG
CAGGCTGAGAAGGTTCTGACATCTGCTCTTCTGTGTTGGAAGGAAGACTTTCAGGGGCGGTTCCGCTGCAGCT
TCTGTGAGCGCAAGAAATGTGGGCTCTGTGCGACAGCAAGGCCAAGGAATGGGACTTGTGCTATTCTTGTCTA
CGGGAGCTGTGTGGAAGAAAGCTGTATGGGACAGATGGAGATAGAGCGCTGCTGGGCAAGCTCCACAGGCGCG
TGCCACGGGACTTGTGCTGAAGAAATAGCAACTCTTAACTGTGTTTCTAGCCGAGCCCACTCCGCAAGAAC
CAGCTAAGAGCTTGTGATGTGTCAGCCAAACGGGGCACTGTGCTCGACAGAGCTAGGGCTGAGAATGTGCC
TGTCTTGGCTGAGTGCAGCAGAAAGTGAACCCCGCTCACAGAGGCCCAAGTGCCTAATCGACACCTCACT
TGTTGGGCTGAGCTGGCTCTACAGTCAGACTTCTCTGTAAAGGTGTCACTGCTTCCGACCTCCACACAGCGC
ATCTTAGGGAAGAGGAGTGTGCCCTATTGGGATTATGGCAAGAAAGTCCAGAGTCGAGCTCGGAGTAGAA
GAGGTGGTGTGTGTTTATCTTGTGATATAAATAAGATGAGTGTGTGGGCTGTCAACACAGAAATCAAGCTC
CTTTGTGATACCGAGCATCTTAAAACTTTGTAGTGTGAAATCTATGACAGAGCAAAATGACTCTGCTGTAACT
TTATTAGAAGAAATTAARAACATGAATCTGGGAGTTCATATTCTTATCACAGGAGCTGGACTGCATCTTCTT
ATAAATGCTTAACACAGCGCGGCTGTGGTGGCTCATGCTGTAATCCGAGCATTTGAGAGGCTGGAGTGGCG
GACTCGCTGAGGTGAGGAATCAAGACGAGCTGGCCAACTGCAAAATGCCCATCTTACTAAAAATAAAAAAA
TTATTAGCTGGAGGTGGTGTGTGCTCTGATTTCCAGCTACTCAGGAGATGAGGCAGGACAGCTGTCTGAAC
CTGGAGGTGGAGTGTGAGTAGGCGAGGTGCACACATCTGACTCTGTGGTAAACAGACGAGCATTTTGAC
AAAAAGGCTTACAACACAGATAGGTAGGACTCAACCAACTGAAACTGACTTCTCCCTGTACCTTCCAGCCGCT
TGCAGTAGTAACTCTTGAGACTCTCCCTGACACGGGACAGCAGCAGGCAATTAGAGCTTTAGATAATAA
CTGGTTTCTTTTAAAAAAAAGAAAAAGGGCGGCGCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
TTTTTTTTTTTTTTTTAAAAAGGGTTTTTTAAAAATCTCCCAACAGATGGCTCTGCAATCTGCCACAGCTC
TGGGCGCTGCTCTGAGGGAAGGCGCTTTTCCCTGAGCGGGCTGGGCTGTGCATGGGTCTCGCGAGCTGT
GCGCTGTCTGGCCTGCGCTGTCTAGCTGCTCTTCTGGGCGACAGAGCTGGGGGTCTGGGGSGCACCGG
AGCTAAGAGCAGGCTCTGTGTCAGGGGTGGAGGCTGTCTTAAACCGACCTTGAGGTGTGCTCTGAGTGTGTG
GGTCAACCTGAGTGCGACGGGAGCAGCTGTGGCGGGTGTCTCTTCTYAGGCCAGCTTGGGAAAGATAAGCTC
GGGCGCTCTTTTGCAAAGACAGGATGGGTGGGTGTGGGGACTATGGGGAATGGCTCTGAGGAGCTACGTGT
GAAGAGGGCGCGGTTTGTGGTGTGACGGCGCTGTGAGCGCTCTCTCTGAGCTCAGTTTCCCTTCTCGGTCTA
ATAAGAGACATTCGCTCTGGTGTCTCAGGCTATTAGAGACTTGCCCTCAGGAATGGCTCTGGACGAGCTGTGAT
GTTATTTTCAACAATCTCTGCGACGTTGGCTGTGGCAGCTCATGAATGGCCGATCTGCTCTCTGCTGTGAC
GTGCGGCTCGGGAGTGTGCGACGACGAGCGGGGCGCAGAGCTGTGCGCTGGGGGTGAGGGGAGGCGCCCGGGAAG
CCTCACAGGAATTTGGGCTCCGCAACACAGCGAGCGGGGCTCCGCGCGGCGCGCCACACCTCTCCAGG
GGCGGCTGACAGAAATGGAATCTCGGCTTGGGCTGCTGTGCGCAGAGTGAACCTTGTATGCAGTGGCGCAGCGG
TGTCTCTGCGAGCTGGAAGCAGGCGCGCTGTACAGCAGCAACAGCGGTGTGCGCT

FIGURE 32

MCFLNKLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC
 CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP
 SLRRTVEFVAERIGSNVCVKHIKATIVADLVRQAESLLQEQLVTQGEEGDPAQLLEILCSQL
 CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIIVGLATEKACAWLSANITAL
 IRREVKA AVSRTLRAQGPAPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGCTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAAACTG
 AAGACTCTCTGCTTTTGCCACAGCAGTTCTCTGCAGCTTCTTGTAGGTGTGAACCCACATCCC
 TGCCCCCAGGGCCACCTGACAGGACGCCGACACCTACCCCTCAGCAGACGCCCGAGAGAAATG
 AGTAGCAACAAGAGCAGCGGTGACGAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA
 GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC
 AACAGACACTGCCCTCTCGGTGCCACCAGTGTGTGATTGTGACGAGCTCCAGCCACCTGCT
 GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGACAAATCCGCATGAATGATGCAC
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCCTACCGCGTCTGTGGCCCATTC
 AGTGTGTTCCGCGTGCTGAGGAGGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGTT
 CATCTTCTGGGGCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCCTGTGATCC
 AGCGAGCGGGCCTGGTGTTCCTCAACATGGAAGCATATGCCGTCTCTCCGCGCGCATGCGG
 CAATTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCGTGGTT
 GAGCACAGGCTGTTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATG
 GCATGGTCCCCCCTAATCTGACGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCACTAC
 TACGAGCCCAAGGGCCGGACGAATGTGTACCTACATCCAGAATGACACAGTGCAGAGGG
 CAACCCACCCGCTTCATCACCCGAGAAAAGGGTCTTCTCATCGTGGGCCAGCTGTATGGCA
 TCACCTTCTCCCACCCCTCTTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG
 AGGAGAAGCAGCCTCCGCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG
 CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCTCCAGCCAATCAGGGCC
 TGGGGAATCTGTGGCGAATCAGGGATTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC
 TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTCTGAGTCAATCTG
 AGGCTAAGGACATGTCTTCTCCATGAGGCCTTGGTTTCAAGCCCCAGGAATGGACCCCCCA
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACTTGGTGTTG
 CCCCCTCAATTTCCAGCACCAGAAAAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGGCC
 GGCCAGAGAAATTTGTGGGGTTGTGGAGGTTGTGGGGCGGTGGGGAGGTCCAGAGGTTGGGA
 GGCTGGCATCCAGGCTTGGCTCTGCCCTGAGACCTTGGACAAACCTTCCCCCTCTCTGGG
 CACCTTCTGCCACACCAAGTTTCCAGTGCAGGAGTCTGAGACCCTTTCACCTTCCCTACAA
 GTGCCCTCGGGTCTGTCTCTCCCCTCTGGACCTCCAGCCACTATCCCTTGTCTGGAAGGCT
 CAGCTCTTTGGGGGGTCTGGGGTGACCTCCCCACCTCTGGAACCTTTAGGGTATTTTTCG
 GCAAACTCTTTCAGGGTTGGGGGACTCTGAAGGAAACGGGACAAACCTTAAGCTGTTTTCT
 TAGCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCCTCTTTCTGCCCT
 CTAGCAGGGAGGTTTTTCAACTGTTGGAGGCGCCTTTGGGGCTGCCCCCTTTGTCTGGAGTCA
 CTGGGGGCTTCCGAGGGTCTCCCTCGACCTCTGTGCTCTGGGATGGCTGTCTGGGAGCTGT
 ATCACTGGGTCTGTCTCCCTGGCTCTGTATCAGGCACTTTAATAAGCTGGGCTCAGTGG
 GGTGTGTTTGTCTCTCTCTCTGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA
 GGCTGGAGGGACAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG
 GGGCGGTGACTGCCCCAGACTGGTTTTGTAAATGATTTGTACAGGAATAAACACCTACGC
 TCCGGA

FIGURE 34

MSSNKEQRS AVFVILFALITILILYSSNSANEVFHYGSLRGRSRRFPVNLKKWSITDGYVPIL
 GNKTLPSRCHQCIVIVSSSSHLLGTLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH
 SSVFRVLRRPQEFVNRTPETVFIFWGPSPKMQKPQGSLVRVIQRAGLVFPNMEAYAVSPGRM
 RQFDDLFRGETGKDREKSHSWLSTGWFTMVI AVELCDHVHVYGMVPPNYCSQRPRLQRMPIYH
 YYEPKGPDECVTYIQNEHSRKGNNHRRFITEKRVFSSWAQLYGITFSHPST

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

GTTTCCTCATAGTTGGCGTCTCTAAGGAAAAACACTAAATGAGGAACTCAGCGACCGGGAGCGACGCAGCTT
 GAGCGAGACCTCCTACTGTTGGCGCAGAGGGCGAGGCTGAAGCGCGAGTGTCTGAGGGGCTTG
 GCGAAGGTGAAAGAGTTTCAAGAACAGCTTCTGGAACCCATGACCCATGAGTCTTGTGCACATTTATACCGT
 CTGAGGTAGCAGCTGAAACTGAAAGAGTGGAGTGTGCCAGGACGGCAGTATCTCTTTGTGTGACCTGGC
 GGCTCTGGGACCTTGGCTTCAGACCTTTGTGATACACC**TG**CTGCGTGGGACGATGACGGCGTGGAGAGGAAT
 AGGCTGTAGGTCACACTGCGTTCCTCCTCCTTAGCCACAGCAGGCTGCTTTGCTGACTTTGAACAGGTTCCCTCAG
 GTCAACGTCACCGCTGCGTCCACGTCAGGAGCCGCGAGGCACTGTGATCTTGGGCTGCGTGGTGGAACTTCCA
 AGGATGAATGTAACTGGCGCTGAATGAAAGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCTCTCATCACC
 CACGGGACCTCTGTCACTACCTGCCCTTAAACAACCACTCTGGGACGGTACAGGTGTGTGGCCCGGATGCTCGG
 GGGCTGTGGCCACGCTGCCACCACTGTGACACTAGCCAATCTCCAGGACTCTCAAGTTAGATGTGCAGCACGTG
 ATTTGAGTGGATGAGGGAACACGACGAGTCATTGCTGCCACCTGCTGAGAGCCACCCCAAGCCGAGGTCCGG
 TACAGGCTCAACAAGAGTGGCTGGAGGCCCTCAGAGGTAACTACCTGATCATGTGCCCTCAGGGAACCTCCAGATT
 GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGACGCTTACAACCCAGTGACCCAGGAAGTGAAAC
 TCCGGCTCCAGCGACAGGCTACGTGTGCGCGCTCCACCGCTGAGGCTGCCCGATCATCTACCCCGCAGAGGCC
 CAACACATCATCGTCACCAAGGCGCAGAGTCTCATTTCTGGAGTGTGTGGCCAGTGGAAATCCACCCCGCAGGCTC
 ATCTGGCCCAAGGATGGGCTCAGTGTCAACGCTCACCGCTACACAAGAGCGGCTTCTCGTGTAGCAACCTCTCATGAC
 ACCACGACGAGGAGGACTCAGGCACTACCGCTGCATGCGCGCAATGGGTTGGCAGCCGGGCGAGCGCT
 ATCTCTCATGATGTCCAGTGTGTTGAACCTCTGAGCTACATGAGACTATCCAGCTGGCTCATCCCTCGGGCG
 CAGAGTGCAGAGCTTACCTGTGAGTGCCTGGGAACCCCGCCCTCGCTGTGTGGCTGAGGAATGCTGTGCC
 CTCTATCTCCAGCCAGCGCTCCGCTCTCCCGCAGGGCCCTGCGCTGCTCAGCATGGGGCTGAGGACGAAGGC
 GTCTACAGTACTGATGCCCGAGAGAGGTTGGGAGCGCCCATGCGGTAGTCAGCTGCGGACCTCCAGGCCAAGC
 AATACCCCAAGCTTATGGCAGATGCTGAGCTGGCTACTGGCACAACCTCTGTATACACCTTCCAAACTCGGCAAC
 CTTGAGCACATGCTGAGGAGGCAACCGCGCTCCCGACCCCAACGTCAGTGGGGCTGCTTCCCCGAGGTGT
 CCAGGAGCAAGGGGCGAGGGGCTCCCGCGAGGCTCCCATCATCTCAGCTCGCCCGCAGCTTCAAAGACAGAC
 TCTATGAACTGTGTGGCGGCTCGGCATGAGGCGAGTGGCGGGCCCAATCTCTATATGTGGTGAACAC
 CGCAAGCAGGTCAAAATTCCTCTGACGATTGGACCATCTCTGGCATTCAGGCAACACGACCGCTGACCTT
 ACCAGACTTGAACCCGGAGCTGTATGAAGTGGAGATGGCAGCTTACAAGTGTGGGGGAGAGGGCCAGACAGCC
 ATGTCTCAGCTTCCGAAGTGGAGCGCGGCCAAACCCGAGATCATGGCCAGCAAGAGCAGCAGATCCAGAGAGAC
 GACCTTCAGGAGCCATCCCCAGAGCAGCAGCCAGACCAACCGCGGCTCTCCCCCAAGAGCTCCGACAGG
 CCCACCATCTGAGGCGCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGAATGTTGGTTCCTCAATC
 CAGTCCCTTCGTTGGAGTACAGAAGCTAAAGAAGTGGGAGACTGGATTCTGGCCACCGAGCCCTCCCCCA
 TCGCGGCTGTGCTGGATACAGGGCTTGAAGAAGGACCTCTTACAAGTTTGAGTCCGGCTCTGAACATG
 CTGGGCGAGCGAGCCCGAGCCCTCTCGGCTTACGTTGTGTGGGCTACAGCGCTCCGCTGTACGAGAGG
 CCGCTGCGAGTCTTATATCACTCTACCGATGGGTCAATGAGACCAACCTCATGCTCAAGTGGATGTACAT
 CGCAGAAGTAAACAACAACCAACTCCATGGCTTTTATATCTATTATCAGACCCACAGACAGTGAACATGATGAT
 GACTACAAGAGATATGTTGGTGAAGGGGCAAGTACTGGCAGCTTCCAGCACCTCGAGCGAGACCTCTCAT
 GACATTAAGATGAGTGTCTCAATGAAGAGGGGAGAGCGAGTTCAGCAACGTTGATGATCTGTGAGACCAAGCT
 CGGAAGTCTTTCTGGCGAGCTGTTGACTGCCACCCCAACTCTGGCCCAACACAGCGGCCCTTCTGGAACC
 ATAGAGCGGCGGCTGGGCACTGGGCGCATGTTGGCTCGCTCCAGGCACTGCCATCTGATTGTGTGGGCTCGT
 CTGGGCTCATCGTTCTCATCATCTGTCACCTTCATCCCTTCTGTTGTGGAGGCTGTGCTTAAGCAAAAACAT
 ACAACAGACCTGGGTTTTCTCGAAGTGGCTTCCACCTCTCGCCGCTATATCTGGTGCCATTGGGAGGACT
 CCAGGCGCCAGGCGAGTGGACAGCCCTACCTCAGTGGCATCAGTGGAGCGGCTGTGCTAATGGATCCCATG
 AATAGGGGCTGCCCTCGGCTGAGTGGGCTACCCGGGCGATGAAGCCCGCAGCAGCATGCCAGGCGAGCTTCAG
 CAGCAGAGTGACACAGCAGGCTGCTGAGCAGACGCCATCTTGGCAATGGATTGACCCCAAGCTCAGCAGT
 ACGAGGGGTCCCAAGTGTAGCCCGGAGGAGGCTTCTTCTATACACTCTGCCAGCTCTCCAGCAGTCTCAGCAGT
 CTGCGGCCCATACGCTCTGCCAGCGGAGGAGAGCTGCTCTGGCGGCTCAGGGGTGAGGAGAGCC
 CCGCAGCTCTCTGTGAGGACCTGTGGGACCTCCATCTCACTCAGGCGCCATGCTGCTTGGGCTTTGTG
 CCGATTGAAGAGGTGGACAGTCTGACTCTCGTCCAAGTGAAGTGGAGGAGCTGGTGTCCCCAGACCCGCTAGG
 CGCTAGTGAAGACAGGAACCTGGAATGCACTCTCCCGGGCCACTGGTGGTGTGTTTGTAAACACCTGCT
 CTCACATTTAGGCAGAGTCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAGAGAGAAAAA
 AGAGACAGGAAAAATGTTATTTTATTTTCTATTATAGCCATTTTATATATTGTATGAATTTAAATAAATGTA
 TATGTTTATAATTCTGGAGAGACATAAGGAGTCTACCGCTTGAGGTTGGAGAGGAAAAAAGAAAGCTGCCA
 CTTAAAGGAGTACCCAGGAAGACCGCACAGGCTGGCGGGACAGACTCTAACTGGGGCTCTGCGATG
 CGAGGCGAGGCTCGAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTTCATCAGAGCA
 TGAGGGGAACAGCAAGGGGACGGTATCACAGCTGGGAGACCCACAGACAGATGGTGGATCCGGTGTACGGGAA
 ACATTTTCTAAGATGCCATGAGACAGACCAAGATGTGTACAGCATATGAGCATATAAAACACTTCCGAGAT
 CAATAATGTCGGCACATATCTCTGAAAAACAACCTGTAACCTTAAATAAATGTTTATGCTTCTCCTGTAAAA

FIGURE 36

MLRGTMATAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQFASVQKPGGTIVILGCVVEPP
 RMNVTVRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVEVDENGTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSGNLQ
 IVNASQDEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEARIIPPPEAQTIIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELSQLVIPWQGSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS
 RRALRVLSMGPEDEGVYQCMANEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGEKQGAPAEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRGTGRPKPEIMASKEQQIQRDDPGASPOSSSQPDHGRLSPEAPDRPTISTASE
 TSVYVTWIPRNGGGFPPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESEPSAPSRPYVVSYSGRVYERPVAGPYITFTDAVNETTIMLKWMIYPASNNNT
 PIHGFIYYRPTDSNDSDYKKDMVEGDYKWHISHLQPETSYDIKMQCFNEGGESEFSNMV
 ICETKARKSSGQGRLLPPTLAPPQPLPETIERFVGTGAMVARSSDLPLYLIVGVVLSIVL
 IIVTFIPFCLWRAWSKQKHTTDLGFFRSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRGCPSAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLNGYDPQSHQITRGPK
 SSPDEGSFLYTLDDSTHQLLQPHHDCCQRQEQPAAVGQSGVRRAPDSPVLEAVWDPPFFHSG
 PPCCGLGLVPVEEVDSPSCQVSGGDWCPQHPVGAYVGQEPGMQLSPGLVRVVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTGGCCCTCTGCCCATCGCCTGCTCCTC
 CCAGGCTCCCGGGCCGACCCCGCGCAAC**CATG**CAGCCCACGGGCGCGAGGGTTCCCGCGC
 GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC
 CCGTAACCCGCGCGGAGACCACGCGGGCGCCCCAGAGCCCTCTCCAGCTGGGCTCCCC
 AGCCTCTTACCACGCGGGGTGTCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG
 CACCCCAAACCTTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG
 TGGACGGCCACAATGACCTGCCCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTCATTACCGCATGTGTGCCTCCTACTCTGAAGTTCGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGTGCCT
 ACCTGACACCTACCTTCACCTGCAGTACACCATGGGCAGAGATTCCACCAAGTTCAGACAC
 CACATGTACACCAACGTGAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA
 CCGCCTGGGCATGATGATAGATTGTCTATGCATCGGACACCTTGATAAGAAGGGTCTGG
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGTGCAGAGCTGTGTGTGACAATTTG
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAATATGACGGGACT
 GGCCGGTTCCCTCAGGGGTGGAGGATGTGTCCACATACCCAGTCTGATAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCTTCGTGGAAACCTGCTGCGGGTCT
 TCAGACAAGTGGAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT
 CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCCTCAGAATGGACACCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCTGGAGGTCCTCAAATGCCT
 CCCCATACCTTGTTCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCAGTGGCTC
 TGCT**GAC**ACAGTCGGTCCCGCAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT
 AGTTCATTACAAGCATATGCTGAGAATAACATGTTACACATGGAAAA

FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALRRYLRRLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSGHQ
TSLDRLRDGLVGAQFWSASVSCSQSDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGGNYDGTGRFPQGLEDV
STYPVLIEELLRSXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFFPYQLSTSCH
SHLVPQNGHQATHLEVTQPTNRVFWRSSNASPYLVPGLVAAATIPTFTQWLC
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCCAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAAGCATG
AAGCTCTTATCTTTGGTGGCTGTGGTGGGTGTTTGGCTGGTGCCCCAGCTGAAGCCAACAA
GAGTTCTGAAGATATCCGGTGCAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
TTTACAACCAGAAATGTATCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCATGCC
GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
CACCACCACCATCAAGGTCATCATTGTCTATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
ACATGGCCTTCTCTGATGCTGGTGGACCCCTGATCCGAAAGCCGATGCATACACTGAGCAA
CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCG
GGGACCCCGAGCAAAACAGACTCTGGAGCTGTGGAAGGTGCCAGCAGCTGGAGCTGC
AGTGCAGGAGCAGCGGAAGACAGCTCTTCGATCGGCACAAGATGCTCAGCTGATAGTGGGTGG
TGTGTTTGGGTCAAGGCCCAACACCTAGGCTGGCTGCGAGCTTCCAGGCTGGACAAGCAGGGGG
CTACTTCTGGCTTCTCTCGGTTCAGTCTTCCCTTTAAAGCCTGTGGCATTTTTCTCTCT
CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTGAAGGGAGGGGAAGGCAGGCCAGAAGGA
ATGGAGACATTCGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCTCGGCTCCACTCTTG
CCGCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGAAGATAAAGCTGGGTCTTCA
GGAACCTAGTGTCTGGGAGAAAGCATGGCCAGCATTCAGCATGTGTTCTTTCTGCAGTG
GTTCTTATCACCACCTCCCTCCAGCCCCGGCGCTCAGCCCCAGCCCCAGCTCCAGCCCTG
AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCACTGGA
AGCTGGTGTTTCGTGTCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT
CTGCTGCCGGTCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCAAGTGTC
CACAGTCACTGAGCCAGACGGTCTGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
CACCACAGCCCCCTGACTTGGGTGCCTCTTGTCCTTGAACCTCGTTGTACCAAGTGCATGGA
GAGAAAATTTTGCTCTTGTCTTAGAGTTGTGTAAATCAAGGAAGCCATCATTAATTTG
TTTTATTTCTCTCA

FIGURE 40

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNSQKDCNCLHVVEPM
PVPGH DVEAYCLLCECRYEERSTTTIKV IIV IYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSM AAAASLGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGGGCTCTGCTTGGGTTCCGCTAATTTCTGTCTCTGAGGCGTGAGACTGAGTTCATAGGGTCCTGGGTCCTCCGA
 ACCAGGAAGGGTTGAGGGAACACAACTCTGCAAGCCCGCGACCCAACTGAGGGGGCCCTGTGTTGGGGTCTCC
 TCCCTTTGCATTCACACCCCTCCGGGCTTTGGCTCTTCCTGGGGACCCCTCGCGGGGAGCTGGCGCGCTTGATG
 CGGAGCAAGGATTCGTCTGTCTGCTCTCTACTTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT
 TCGCGGGCCAACTCAACTCCATCAAGTCTCTCTGGGCGGGGAGACGCTGTGTCAGGCCCCCAATCGATCTGGC
 GGCATGTACCAAGGACTGGCATTCGGCGGCGAGTAAGAAGGGGCAAAACCTGGCGGACCGGCTTACCCCTTGTAGCAGT
 GATAAGGAGTCTGAAGTTGGGAGGATTGGCACAGTCCCCACCAAGGATCATCGGCCTGSCATGCTGTGTGCGAGA
 AAAAAGAGCGCTGCCACGGAGATGGCATGTGCTGCCCCAGTACCCTGCAATTAATGGCATCTGTATCCGAGTT
 ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCGAGGTCATTAC
 TCAAAACCATGACTTGGGATGGCAGAACTTAGGAAGACCAACACTAAGATGTACACATATAAAGGGCATGAAGGA
 GACCCCTGCTACGATCATCAGACTGCATTGAAGGGTTTGTCTGTCTCGTCATTCTTGGACCAAAATCTGCAAA
 CCAGTGTCTCCATCAGGGGGAAGTCTGTACCAAAACACGCAAGAGGGTTCTCATGGGCTGGAAATTTTCCAGCGT
 TGGCAGTGTGCGAAGGGGCTGTCTGCAAAAGTGAAGAAGTCCACCTACTCTCCAAAGCCAGACTCCATGTG
 TGTGAGAAATTTGATACCACTTGAAGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG
 CATGGTGGAAATAAGGTTCAGATCGAGAAGATGGCTAAAATAAGAAACGTGATAAGAAATATAGATGATCAAA
 AAGGGGAGAAAGAAACATGAAGTGAATAGATAGAAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG
 CAACTTGTCTATGTAAATATGTACACATTTGTGGAAATGCTATTATTAAGAGAACAGCACAGCTGGAAAT
 ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTCTGGAGGAGAGGTTTCCCTCAGATGCTGATTGC
 TTATACAAATAACCTACATGCCAGATTCTATTCAACGTTAGAGTTTAAACAAATACTCCTAGAATAACTTGTGA
 TACATAGGTGCTAAAATAAATTTGCTAAACAAGAAATGAAACATGGAGCATTTGTAATTTACACAGAGAAAT
 TACCTTTGTATTGTAAACACTCTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAATCAGTCAATAT
 TCTCAAATAATTTGCAAAATAATGGCCAGTTGTTTAGGAAGGCTTTTAGGAAGACAAATAAATAACAAACAAACAG
 CCACAAATACTTTTTTCAAATAATTTAGTTTTTACTGTAAATTAAGAAGCTGATACAGACAAAAACAGTCC
 TTCAGATCTACGGAATGACAGTATATCTCTTTATCCTATGTGATTCCTGCTGGAATGCATTATATTTTCCA
 AACATATACCCATAATTTGTGACTAGTAAATACTTACACAGACAGAAATTTACAGATGGCAAAAAATTTAAAG
 GATGTCGAATATATGTGGGAAAGAGCTAACACAGAGAGATCATTAATTTCTTAAGACTTGGCCATAACCTATATTT
 GATAGAATTAGATTGGTAATACATGTAATTCATACACTCTGTGGTAACAGACTTAAGCTGAGTCTGTACTG
 CACTGGAGTAGCAAGAAATTTGGGAAACCTTTTCTGTTGTTCAGGTTTGGCAACACATAGATCATATGCTG
 AGGCACAAGTTGGCTGTTTCATCTTGAACACGAGGGATGCACAGTCAAAATGAATATCTGCATGGGATTTGCTAT
 CATAAATATTTACTATGAGAGATGAATTCAGTGTGAGTCTGTGCTCGTACTATCTCTCAAATTAATTTATTTATAG
 TGCTGAGATCCTCAAATAATCTCAATTTCAAGAGGTTTACAAAATGTACTCTGAAGTAGACAGAGTAGTGAGG
 TTTCAATGGCCCTATAAGGCTTCTGACTAGCCAAATGGCATCATCCAAATTTTCTTCCAAACCTCTCGCAGCATCTG
 CTTTATTGCCAAAGGGCTAGTTTCGGTTTTCTGCAGGCATTGCGGTTAAAAAATAAAGTAGGATAACTTTAACT
 ACCTGCATATTGCTAATCTATAGACACCAAGTTTCTAAATTCCTTGAACCCACTTTACTACTTTTAAACT
 AACTCAGTTCTAAATACTTTGCTCGAGCACAAAAAATAAAGGTTATCTTATAGTCTGTGACTTTAACTTTT
 TAGACCACAAATCATTCTTTAGTTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCAGTAG
 AGATTGAGTTGAGCCTGTATATCTATTAATAATTTCAACTTCCCACATATTTACTAAGATGATTAAAGACTTA
 CATTCTTCACAGCTGTCGAAAAACAAAAATATAAACTAGTCCATCCAAGAACCAAGTTTGTATAAACAGGT
 TGTATAAGCTTGTGAATGAAATGGAACATTCATCAAACTTTCTATATACAATTAATATATTACAAAT
 TTGTTTCTGCAATTTCTTTTCTTATGTCCACCCCTTTAAAAATTAATTTTGAAGTAATTTATTGAAGGAAATG
 TTAATGAGATGTAATTTCTTATAGAGATATTTCTTACAGAAAGCTTTGACAGAGATATATTGACAGTATTGAC
 TTTGTAATTTAGAAAAATGTATAAAGATAAACTCTAATAATTTTCTCCTCTAAAAACCTGAAAAAATAA
 AAAAAAATAAATAAATAA

100121-5-241001

FIGURE 42

MAALMRSKDSSCCLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLGQAYPCSSDKECEVGGRYCHSPHQSSACMVCRRKKRCHRDGMCCPSTRCNN
GICIPVTESILTPHIPALDGTNRHRDRNHGYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS
SDCIEGFCCARHFWTKICKPVLHQGEVCTQRKKGSHGLEIFQRCDAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

42/249-2-2004

FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAAATCCACCTACCTTGGCCTCCCAA
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGCCAACATCACGTTTTTAAAAATTGATT
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA
 TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATAC'TTGTGAAAACTACTG
ATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTGTTCTTTTATCCCCCT
 TTTAAAGTCATCCGTCCTTGGCTCAGGATTGGAGAGCTTGCAACCACCAAAAAATGGCAACA
 TCACCAAGCTCCCGAGATTTTGACCAAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCCACAACTACTACTTCTTGGGACCTCAAGCC
 CCCAACATCCCAAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTAACCTGAGCCATCCC
 CAGTTCCTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCTCTCT
 CCTGGTTTGGAGTCCTTTCTTCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCC
 CTCCACTGTGAACAAGCTTTTGACGCTTCCAGCAGCACCATTGAAAATATCTCTGTGTCTG
 TCCACCAGCCACAGCCCAACACATCAAAC'TTGCTAAGCGGCGGATACCCCGAGCTTCTAAG
 ATCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAATGTGCAGTT
 TGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATTTCCATCAGCTTGATTGCAAGTCTTTAAGTGAGCCTTTGAATACA
 TCTTTATCAATGACCAGTGCAGTACAGAATCCACATATACAACCTCCGTATTACCTCCTG
 CAGTCTGACAAGCTCATCACTGAATCTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCATACCAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA
 GGAACCATCATGAATGGACATGGTGGTGGTTCGAAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTGTGCATGGCTGGTGCCAACCAACAGAGGAAGAGGATAGCTCACGTGA
 TGTGGAACACCAAGTTGGTCAATGGCTCATTGCTTAAAGCAGCCCTTTTGCTTTTTTGT
 TTTTGGACCAAGTGTTGGCTGTGGTGTTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
 GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTCGACATACAGTATGCAT
 TTTAAAGATGCTTGGGCCAGCGGGGTGGCTGATGCCATAATCCCAAGTGCTTTGGGGGGCC
 AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACCACCTGGGCAACATGGTGAAACTG
 TGTCTCTACTAAAAACGAAAAACTAGCCGGGTGTGGTGGCGGCGGTGCCTGTAATCCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
 GTCTGAAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP
GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVPTKQRKRIAHVMWKTTPVGQWLIR

Signal peptide:

amino acids 1-24

FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCC**ATG**CGCGTGCCATCCCGAATCCTGCT
 TTGGAAACTTGTGCTTCTGACAGACTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCGCCCTGGAGGTACCGACGCGCCCCCGGCCACCCCGCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGGGCGCACCCGCGCTTCTGACCTGCGTGAACCGCGGCACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGCGGACCGGCAGCCGCCCGGG
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTGGGCGAGCGCCGCGCCTA
 CGGGCCCCCTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCCCGCTCTTCCACCTGACGGTCGCGGAACCCACGC
 GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGCGCCCCAGGCCCAG
 ACCCCACACTGGCGCGCGGCCACAACGTATCAATGTATCGTCCCCGAGAGCCGAGCCCAC
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTTTATCCTGCTACTGGTCA
 TGTCTCTTGGCGCCCGCAGCGCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACTCCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAAGGGTTCGGAAGGAGAACT
 GCAAA**TAG**GGAGGCGCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTCGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCCT
 GGAATTTGGCCTGGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC
 AGCATAGCCCCACCCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAAAC
 AAAATCCACTGATGCCATCATGCCCTCAGACCCTTCTGGGCTCTGCCCGCTGGGGGCTG
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAATGGGGTCAGCCTCA
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGCTGGGAGATGTTCTTGAGGA
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT
 CCTCTGGGGTGCTGCCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTCTCTGCCCATCCCTACCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCTGACACCCCTCCCTT
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA
 CAGGGGAGGGAGTGAAGTTGTTTGGGGTGGCCTGTGTTGCCACTCTCAGACCCACATTT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTAAAAA
 AAAAA

FIGURE 46

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHRVVEAQVQVHWRQPPGVPHDRADRLDL
YASGERRAYGPLFLDRVAVGADAFERGDGFSRLRIEPLVADEGTYSCHLHHHYCGLHERRVF
HITVAEPHAEPPIRGSPGNGSSSHGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPKAYIDLDKGFRKENCK

Important features:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGCGCGCTGGCGCAGCGGCACATGGCCGTTGTCTCAGAGGACGACTTT
 CAGCACAGTTCAAACCTCCACCTACGGAACCAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
 ACTGCTTGAGAAGCTGCTGGACCGCCCGCCCTGGCCTGCAGAGGCCCGAGGACCGCTTCT
 GTGGCACATACATCATCTTCTTCAGCCTGGGCAATTGGCAGTCTACTGCCATGGAACCTCTTT
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGGCCACCGGGGA
 GGACCTTGAGGGCTCAGACATCCTGAACCTACTTTGAGAGCTACCTTGCGTTTGCCCTCCACCG
 TGCCCTCCATGCTGTGCTGTGGCCAACTTCTGCTTGTCAACAGGGTTCAGATCCACATC
 CGTGTCCTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATACTGCTGACTGGTGA
 GGTGGACACTTCTCCTGGACCCGTGGTTTTTTTGCGGTCACCATTTGCTGCATGGTGATCC
 TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCTATG
 AGGAACCTCCCAAGCACTGATATCAGGAGGAGCCATGGCGGGACGGTCAGCGCCGTGGCCTC
 ATTGTTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG
 CCACCATCTTCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC
 AGGTACTACATGAGGCCTGTTCTTGCGGCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCA
 GGACTCCCTCAGTGCCCTTCTGGTGGCCTCCAGATTCAATTGATTTCCACACACCCCCCTCTCC
 GCCCCACTCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTCACCTACGCTCTTCTTCATCACC
 AGCCTCATCTACCCCGCGCTGCAACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT
 GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCTCCTGTACAACCTTTGCTGACCTAT
 GTGGCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCCTCCAGGG
 TTCGTGCTCCTCGGACCTGCCTCATCCCTCTTCTGCTGCTGTAACTACAGCCCCGCGT
 CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCTGTGCTGG
 GGCTCAGCAACGGCTACCTCAGCACCTGGCCCTCCTCAGCGGCTAAGATTGTGCCAGG
 GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCTTTTATGTGTCTTGGGCTTAACACTGGG
 CTCAGCTGCTCTACCTCCTGGTGCACCTCATCTAGAAAGGGAGGACAAAGGACATTGGTG
 CTTTACAGGCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCC
 TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCTCATCCCTCCCAAGATGCCA
 GTGAGCCAGTCCATGCCATTCCTGCAAGGCAGATATTCCAGTCAATTAACAGAACACT
 CCTGAGACAGTTGAAGAAGAAATAGCAAAATCAGGGGTACTCCCTTACAGCTGATGGTTA
 ACATTCACCTTCTTTTAGCCCTTCAAAGATGCTGCCAGTGTTGCGCCTAGAGTTATTACA
 AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCAGCTGCGCTCATTCAGCT
 GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCTTACCTGAAGGGGTCTCCTTGAATGGA
 AGTCCCTGGCATGTTGCTCCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
 GCGGGTGAACAACTGCCACTAACCCAGACTGGAACCCAGAAAGATGGGCTTCCATGAAT
 GCTTCATTCAGAGGGACGAGGGCCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
 TTTTCAAAAAAGAGGGATCCTCATGACCTGGTGTCTATGGCCTGGGTCAAGATGAGGGTC
 TTTCACTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGCGTAATAAATACTTGC
 GTATTCAAAA

FIGURE 48

MAVVEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGQLQRPEDRFCGTYIIFFSLGI
 GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
 LVNRVAVHIRVLASLTVILAIFMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
 YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFVLVCMGLY
 LLLSRLEYARYYMRPVLAHVFSGEEELPQDSLAPSASVSRFIDSHTPPLRPILKKTASLGF
 CVTYVFFITS LIYPAVCTNIESLNKGSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
 GPNSKALPGFVLLRTCLIPFLVLCNYQPRVHLKTVVFSQSDVYPALLSSLLGLSNGYLSTLAL
 LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
 305-330, 448-472

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCTGCTGTACCAAGAGCTGGAGACACCA
 TCTCCCACCGAGAGTCA**ATG**GGCCCCATTGGCCCTGCACCTCCTCGTCTCGTCCCCATCCTCC
 TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGTGCTGACCTGGGGGCTCAATCGGACCCT
 GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC
 TCAGCGATGCTGGACACAAGGTCAACATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAG
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTCACCC
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
 AAGGTGCCCGAGAAGCTGGGCTACGCCTTGCGTCCCCAGGAAAAGGGCCACTCGCCGAAGA
 CATCTACCAGATGGCTCTCAACAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG
 CGATGAAGAAGTTTGAAGGCACACGCTCTTGAATATCTTCTCGGGGAGGGGAACCTGAGC
 CGGCCGGCCGTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT
 CGCCGAGGCCCTCCGGGCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG
 GTGGCTGGGACCTGCTGCCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAAC
 GCGCCCGTGGTGGCGATGACCAGGGACCGCACGATGTGCAGTGCAGATCGAGACCTCTCC
 CCCGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGG
 CGGTGAAGCGCATCACCTTCTCGCGCGCTGCCCGCCACATGCAGGAGGCGCTGCGGAGG
 CTGCACTACGTGCCGGCCACCAAGGTGTTCTAAGCTTCCGCAGGCCCTTCTGGCGCGAGGA
 GCACATTGAAGGCGGCCACTCAAACACCGATCGCCCGTTCGCGCATGATTTTCTACCCGCCG
 CGCGCAGGGCGCGCTGCTGCTGGCTCGTACACGTGGTCGACGCGCGCGCAGCGTTCCGC
 GGCTTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC
 TGTCTGTGCCAGCTCTGGGACGGCACCGGCGTCTCAAGCGTTGGGCGGAGGACAGCACA
 GCCAGGGTGGCTTTGTGGTACAGCCCGCGGCGCTCTGGCAAAACGAAAAGGATGACTGGACG
 GTCCCTTATGGCCGCATCTACTTTGCCGCGAGCACACCGCCTACCCGCACGGCTGGGTGGA
 GACGCGGTCAAGTCGGCGCTGCGCGCCGCATCAAGATCAACAGCCGAAGGGGCTGTCAT
 CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGACGGGCATGTGCATGGG
 GTGGCCAGCAGCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCTCCAGTCCAAGG
 CCAGTTATCTCTCAAAAACAGACCACACGAGGACCTCGCAT**TAA**AGTATTTTCGAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 50

MAPLALHLLVLPILLSLVASQDWKAERSQDPFEKCMQDDPDYEQLLKVVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLS DAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLG YALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMS EDGFFYLSFAEALR
AHSCLSDRLQYSRIVGGWDL LPRALLSSLSGLVLLNAPV VAMTQGP HDVHVQIETSPPARNL
KVLKADVLLTASGPAVKRITFS PPLPRHMQEALRRLHYVPATKVFLSFR RPFWREEHIEGG
HSNTDRPSRMIFYPPPREGALL LASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL
WDGTGVVKKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHG VASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAT
 GCACGGCTCTGAAGCCACCCCTGTCTCTGGAGGAACACAGAGCGAGGAAGAGACAGGAGACTCGTGTGGCAGGAA
 GAACCTCAGAGCGGGGAAGCCCCCATTCACCTAGAAAGCACTGAGAGATGGCGGCCCTCGCAGGGCTCGTAATTCCT
 GCTGCTGTTCACAAAGATGCTTTTATCTTTAACTTTTTGTTTCCCACTTCGACCCCCCGGGCTTGATCTGCAT
 CCTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACCAGACCTCAACCCGCTTTACCTCTTCTTGACCTGAA
 CAATCAGCTCTGGGAATTGAGGGAGGAGCAGGAAGGGGGTTTCCAGAAAGCAACATGACCTAAACAAGTTGCTG
 CTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAGGACTCGCTGTGCTGACAAATGGGCCCTGCTTGGG
 ATATAGAAAACCAACAGCCCTACAGATGGCTATCTTACAAACAGTGCTGTATAGACAGAGTACCTGGGTTC
 CTGTCTCTTGCATAAAGGTTATAAATCATCACCAGACGATTTGTCCGCATCTTTGCTCAGAATAGGCCAGAGTG
 GATCATCTCCGAATTTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAAGC
 CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAGGCATTTGGTGTGAT
 AGGGAATGTAGAGAAAGGCTTCAACCCGAGCCTGAAGTGATCATCCTTATGAGCCCTTTGTATGATGACCTGAA
 GCAAGAGGGGAGAGAGATGGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAGAGCACTTCAG
 AAAACCTGTGCCTCTAGCCCCAGAGCCTGAGCGTCTATGCTTCCACAGTGGGACCACAGGTGACCCCAAGG
 AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTGCTTCTTCAAATGTGTGGAGCATGCTTATGAGCC
 CACTCTGTATGATGTGGCCATATCTACCTCCCTCTGGCTCATATGTTGAGAGGATGTACAGGCTGTTGTGTA
 CAGCTGTGGAGCCAGATTTGGATTCTTCCAAAGGGATATTGCGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
 CACATGTTTCCCGCGGCTGCTCGACTCCTTAACAGGATCTACGATAGGTACAAATAGAGCCAAAGACACCCCT
 GAAGAAGTTCTTGGTTGAAGCTGGCTGTTTCCAGTAAATCAAGAGCCTTCAAAGGGATCATCAGGCATGATAG
 TTTCTGGGACAAGCTCATCTTGTCAAAGATCCAGGACAGCCTGGGCGGAAGGGTTCTGTATTTCTACTGTGACT
 TGCCCCCATGTCCACTTCAGTACATGACATCTTCCGGGCAGCAATGGGATGTATGAAGCTTATGGGCTCA
 AACAGATGCACAGCTGGCTGTACATTTACATTAACCTGGGACCTGGACATCAGTCACTTGGGCTGCCCTGGC
 TGTCAATTTACGTGAAGCTGGAAGATGTGCGTGACATGAACCTTTACAGTGAAATATGAAGGAGAGCTTCGAT
 CAAAGGTACAACCTGTTCCAAAGATACCTGAAGGACCTGAGAGACCAAGGCCCTGGACAGTGATGGCTG
 GCTTCACACAGGAGACATTTGGTCCCTGGCTCCCGATGGAACCTCTGAAGATCATCAGCCGTAAAAAGAACCTTT
 CAAAGCTGGCCCAAGGAGATATGTCACCCAGAGAGATAGAAAATATCTCAACAGGAGTCAACAGGATTTACA
 AATTTTGTACACGGGAGAGCTTACCGCTCATCCTTAGTAGAGTGGTGGTTCTGACACAGATGTACTTCCCTC
 ATTTGACGCCAAGCTTGGGCTGAAGGGCTCCTTTGAGGAAGCTGTGCCAAAACCAAGTTGAAGGGAAGCCATTT
 AGAAGACTTGCAGAAAATTTGGGAAAGAAAGTGGCCTTAAAACCTTTGAACAGGTCAAAGCCATTTTCTTCACTC
 AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTTCCAAATCTT
 TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGGCCAGCT
 TGCACCTGCTGTGAGAAAATGGATTAAAAACATTTCTTACATTTGTTTGGCTTTCCTCCTATTTTTTTTAAAC
 TGTTAAACTCTAAAGCCATAGCTTTTGTTTTATATTGAGACATATAATGTGTAAACTTAGTTCCTCAATAATCA
 ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAAGGCTTCAGGGCTCATTTTATCAACATGCCTGTCTTCAA
 GATCCAGTTTATGTTCTGTGCTTCTCATGATTCCAACCTTAATACTATTAGTAACCAAGTTCAAGGTT
 CAAAGGGACCCCTCTGTGCCTTCTTCTTTGTTTGTGATAAACATAACTTGCCAAACGCTCTATGCTTATTTACA
 TCTTCTACTGTTCAAACTAAGAGATTTTAAATCTGAAAAACCTGCTTACAATTCATGTTTCTAGCCACTCCAC
 AAACCATCAAAATTTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAATGTCTCCGATGCTCTT
 CTGCGTAATTAATTTGTGTACTGAAGGGAAAAGTTGATCATACCAACATTTCTCAAACTCTCTAGTTAGATA
 TCTGACTTGGGAGTATTAATAATTTGGGCTATGACATCTGTCCAAAGGAATGCTTCTTAAGAGCATTAATTA
 CAGTAGGAAGCTGGGAGATAAATCTGTCCCTACAGTTTGTGCTGAGCTGGAAGCTGTGGGGAAGGAGTGA
 GGTTGGGCCAGTGAACCTTTTCCAGTAAATGAAGCAAGCACTGAATAAAAAACCTCTGAACCTGGGAACAAAGATCT
 ACAGGCAAGCAAGATGCCACACCAACAGGCTTATTTCTGTGAAGGAACCAACTGATCTCCCCACCCCTTGAT
 AGAGTTCTGCTCTACCTTACCACAGATAACACATGTTGTTTCTACTTGTAAATGTAAAGTCTTTAAATAAAC
 TATTACAGATAAAAA

FIGURE 52

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<MW: 82263, pI: 7.55, NX(S/T): 3
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FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPPLDLNNQSVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVFQRGBLAVSDNGPCLGYRKPNQPYRWLSYQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIIIMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIIVSNAAFLKCV E HAYEPTPDDVAISYLP LAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFELQKGIIRHDSFWDKLIFAKIQDSLGGRRVRVITGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHVGVPACNYVKLEDVADNMNYFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDSGWLHTGDIGRWLFNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR
SQPVLQIFVHGESLRSSLVGVVVPDPTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAI FLHPEPF SIENGLLTPTLKAKRGELSKYFRTQIDSLYEHIQD

```

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

FIGURE 54

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
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REQQGGIHHVIVLNQATGHVMAKRVFDITYSPHEDEAMVLFILNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSAQGPALGWRDWTAFVGRKGGPVFGEKHSKSPALSSWGDVPLLKTDVPLSS
AEEAECHWADTELNRRRRRFC SKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNYLYRMLRSLLSAQGVSPQMITVFIDGYEEPMDDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPFAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRSLYKEELEPKWPTPEKLWDWDMWMMRPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTPVPGVQLRNVDLSLKEAYEVEVHRLLEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLVVRGNHRLGLRFLFRKKNH
FLVVGVPASPYSVKKPPSVTFIFLEPPPKEEGAPGAPEQT
```

Important features of the protein:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAGGCCACTCTCTTGGAAACCACCACAC
 CTGTTTAAAGAACTTAAGCACCATTAAAGCCACTGGAATTTGTTGTCAGTGGTTGTTGGGTGAATA
 AAGGAGGGCGAGAATGGATGATTTTCATCTCCATTAGCCTGCTGCTCTGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAATCATTTCCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTGG
 GTGCTGGCCTTCTCTGTGGAACGTCTGGCAGTCTATCGTGCCTGAAGGATGATGCCCTTTATGAA
 GATATTTCTGAGGGAACACCACCAAGCAAGTGAACACATAATGTGATTGCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCATGAACATGAGCACAGCCAGCACCACACAGCTGCATGCCCTATATTGGTG
 TTTCCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACAGATTGGTAACCTCCATGTGCAATTC
 ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCAAAAATCACCACCAGCTGGGTCTGGTTGTCCA
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTF
 GTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCTTCTTGATGCATGCT
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCAATGGCAGCACCAGTTATGTCCAT
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAAGCCCTTTCAGAGGTGAAGCCACAGGGAGTGG
 CCATGCTTTTCTCTGCGCGGACATTTCTTTATGTTGCCACAGTACATGTCTCCTCCTGAGGTGGGCGGA
 ATAGGGCAGCGCCAGGCCGATGCCACGGGAGGGAGAGGCCCTCAGCCGCTGGAACTGGCAGCCCT
 GGTTCGTGGTTGCTTCCTCTCCTCCTGTCAGTAGGACACCAGCATTAATGTTCAAGGTCCAGC
 CTGGTCCAGGGCCGTTTGGCCATCTCAGTGAGAACAGCCGCGCAGTGCAGCTACTCACTTCTCATGCT
 TCTTGTCTCACCTTGGCGCATCTCTACATGTATTCTAGAGTCCAGAGGGAGGTGAGGTAAAAACCTG
 AGTAATGGAAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTTGTGT
 TATCTTTTAAAGGCCCTTGACATTTTGCCTTTAATATTTCTCTTAACCTATTTCTCAGGGAAGATG
 GAATTTAGTTTTAAGGAAAAGAGGAGAACCTCATACTCACAATGAAATAGTGATTATGAAAATACAGT
 GTTCTGTAATTAAGCTATGTCTCTTTCTTCTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTT
 AACATGTTCCACCATGTAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTCATA
 GCACCCACTCACTTAGTCTAGCTAAAGGTGATTCTAGTTAATCTGGGATGAGGACAGGAAATGATAGC
 AAGACACATTTGAAAGCTCTCTTTATCTCAAAGAGATATCCATTGAAAGGGATGTCTAGAGGGATT
 TAAACAGCTCCTTTGGCAGCTGCTCTCTGAATCCAGCCTGCCATTCCATCAAAATGGAGCAGGAGAGG
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTGTAGCATTCCCTGTCAAGTCTCCTTTGCAGAAAT
 ACCTGTCTCCACATTTCTAGAGAGGAGCCAAAGTTCTAGTAGTTTCAGTTCTAGGCTTTCCCTCAAGAA
 CAGTCAGATCACAAGGTGCTTTTGGAAATTAAGGGATATTAATTTTAAGTGATTTTTGGATGGTTAT
 TGATATCTTTGTAGTAGCTTTTTTTAAAGACTACCAAAATGTATGGTTGTCTTTTGTGTTTTT
 TTTTTTTTAAATTTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTCAGCTTT
 GGCACACTGTGTCTTCTACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTTTGCCTA
 TGTATTTAAAGCTTATTGGAATCATGTCTTGTCTCTCTGCTTTTCTTGTGCTTTCTCTTAACCTT
 TCCCTCTAGCCTCTCCTCGCCACAATTGCTGCTTACTGCTGGTGTAAATATTGTGTGGGATGAATT
 CTTATCAGGACAACCACTTCTCGAATGTAATAATGAAGATAAATATCTTTATTTCTTTATCCCTT
 CAAAGAAATTAACCTTTGTGTCAAATGCCGCTTTGTGAGCCCTTAAATATACCACCTCCTCATGTGTAA
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 TCTTCAGGCGAGTGGACGTAGTAGTTTGTAAAACGTTTTCTATGACGCATAGCTAGCATGCTCATG
 ATTTATTTCTCATGAATTTGTCACTGGATCAGCAGCTGTGGAAATAAAGCTTGTGAGCCCTGTGCT
 GGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCAATTTGGCAACATTTGCATACA
 ATTTTACTACCAAGAGAGGTATAGTATGGAAAGTCCAAATGACTTCCTTGTGGAATGATTAACAGCT
 GACTGGTGTGAGACTTGAGGTTTCATCTAGTCCCTCAAACATATATGTTTGCCTAGATTCTCTCTGGA
 AACTGACTTTGTCAAATAAATAGCAGATTGTAGTGCAAAAAAA

FIGURE 56

MDDFISISLLSLAMLVGCYVAGIIPAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ
IGNSHVHSTDDPEAARSSNSKITTTGLVHVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLVVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILLSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

GCTCGAGGCCGGCGGGCGGGAGAGCGACCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC
 CGAGTGGCGGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCGGCCCTGGTGGCTGCGATC
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGAGCGTGGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGCTCCGAGGGCGGCTGCAGAGAGAGGCGCGCTGGAGCTGAAGA
 AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
 CACAACTTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGCGGTTTTGGTGAA
 TAACATCACACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCGATTAAAGACCCCTGCAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG
 AGGAAGTTCTCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTCAACAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
 GCAGCAGGCTGCCACACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGGTAACAGCAA
 GTCCCAGACACCAGCCCCAGTTCCGAAGTGGTTTTGGATTCAAAGAGACAAGTTGAGAAAAG
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG
 CCAGGCCGGGAGCAGGTGGTGAAGACAGACCTGTAGGTGAAGAGGCTTCGGGGGAGCCGG
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCTAGTGAGCCAGGAAAATCCAGAGA
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 AATCATACACTCTGAATTGAACTGGAATCACATATTTACAACAGGGCCGAAGAGATGACTA
 TAAAAATGTTATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATCTGA

FIGURE 58

MMGLGNRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAAERGA
 VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
 KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
 SRDLSENNDQRQQLQALSEPQPRLQAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLDSCR
 QVEKEETNEIQVVNEEFQDRDLPQEPGREQVVEDRPFVGGRGFGGAGELGQTPQVQAALSVSQ
 ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGND
 RNIDVFNVEDQKRDITINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

FIGURE 59

GGATG CAGAAAGCCTCAGTGTGCTCTTCTCGGCTGGGCTGCTTCTCTTCTACGCTGGCATGCGCTCTTCA
CCAGTGGCTTCTGCTCACCCTTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCAGGCGCTGGGTCCT
TGCCATGGGGAGCCAAAGGAACCTGGGGCTTCTGGATGGCTCCCGATTTTCCGGGGTGTGTTTGGTGCTGA
TAGATGCTCTGCGATTGGACTTCGCCACGCCCCAGCATTCACACGTGCTTAGAGAGCGCTCTGTCTCCCTACCTCT
TCCTGGGCAAACTAAGCTCTTGCAGAGGATCTGGAGATTACGCCCAACCATACCGGGCTCTACCGATCTCAGG
TTGACCTCTCTACCAACCCATGCGAGCGCTCAAGGCCCTCACCACTGGCTACTGCCTACCTTTATTTGATGCTG
GTACTAACTTCGCCAGCCACGCCATAGTGAAGACAATCTCATTAAAGCAGCTCACCAAGTGCAAGGAAGCGGTAG
TCTTCATGGGAGATGATACCTGGAAAGACCTTTCCCTGGTGCTTCTCCAAAGCTTCTCTTCCCATCTCTCA
ATGTCAGAGACTAGACACAGTGGACAATGGCATCTGGAAACCTCTACCCACCATGGACAGTGGTGAATGGG
ACGTGCTGATTGCTCACTTCTGGGTGTGGACCATGTGGCCACAAAGCATGGCCCTCACCACTGAAATGGCCA
AGAACTTAGCCAGATGGACAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG
CTGGGGACCATGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTCAGCTGCTCTCTTTC
TGATAGCCCCACAGCAGTCTTCCCGACACCCACAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCCTTGTGC
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CCTCTCCCTGGCTGAGTCTCTGGCAGTCCATGGTGGGTGGTTCAGGACAGAAATTTATGATGAGCTGTGTGTG
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TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGTGGTGAAGGCTGGGCGAGGCGCTCAA
GGACAGGACTGTCTCACTCCCTTCTCAGGCCCCCCACTTCTCAAGCTGACTGGATTATGTGGTCCCTCAA
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TGATGCGGAGCGCATCAGCCTTGTGTCTGCTCTGTTTCTGCAAGAGCTTCTCTCTCACTCTGTTGCTGTG
CTGGGATACCGTACCACCCCTGGTCTTTTACTGTGCCATGGCAGGCACTCTCGGCTTGGGCCCTCATGGCCA
CAGACCTTCTACTCCACAGGCCACAGCCTGTCTTCCAGCCATCCATTGGCATGCAGCCTTCGTGGGATTC
CAGAGGCTCATGGCTCTGACTTGGCTGCTGCTTGTCTAGTGGGAGCAACAGCTTTGCTCGCCCTCCACTCTCT
TTGCAATAGGTTGCCACTGCTCTGCTCTGGCTTCTCTGTGAGAGTCAAGGCTCGCGAAGAGACAGCAGC
CCCCAGGAATGAAGCTGATGCCAGATCAGACCCGAGGAGGAAGGAGGCCACTGGAGATGCGGCTCGGGCTCGGG
ATCGGCTCAGCACTTCTATGCAGACTGCTCAGCTGGGCTCAAGTACTCTTATCTTGTGATTCAGATTGCT
TGCCCTGTGCTTGGCAGCTCCATCTTGCAGGCACTCATGCTTCTGGAAAGTGTGGCCCTAAGTTCATAT
CTGAGGCTGTGGCTTCAATTGTGAGCAGCTGGGACTTCTCTGGGCACTAGCTTTGGTGATGAGAGTGGAATGGT
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TCTTACTATCTGACGCCAGGGGGCGCTGACATCTAGGACTTCAATTTCTATAAATTCAGGACACAGTGGAGTA
TGATCCCTTACTCTGATTTTGGATGACTCTGAGGACACAGGGGGCGGTCTCCGAAGTGGAAATAAATAGGCGGC
GGTGTGACTGTGACCTATAATCCAGCACTTTGGGAGCAGAGGTGGGAGGATTCCTTGGTCCAGGAGTTCA
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FIGURE 60

```

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VDPPTTTMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMDGDDTWKDLF
PGAFSKAFFFFPSFNVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVHDCHGKHGPHHPPEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGTTNGDHGGDSELEVSAAFLYSPATAVFPST
PPEEPEVIPQVSLVPTLALLLGLPIPGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ
QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAI SPGFPCPLLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLGAVAAVSSFLPFLWKAWAGWGSKRPLATLPPIPGPVLLLLLFLRLA
VFFSDSFVVAEARATPFLLGSFILLVVLHWEQQLPPKLLTMPRLGTSATNPPRHNGAY
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRLVVS GASMVL P
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLETKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLFLQSFL
LLHLAAGIPVTTGPGFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHAAFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLLCESQGLRKRQPPGNEADARVRPEEEEEP
LMEMLRLDAPQHFYAALLQLGLKYLFI LGIQLACALAASILRRHLMVWKVFAPKFIFEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

```

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGCGCCTTGGGGACGGGCAGTTCCTGT
 GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAAATTGGCCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT
 CCTGACAGCTCCAGAGAAGTGAAGAGAAATCCAGAAGACCTTCCCTGTTTCCATGCAACAAA
 TATACTCCAATCTGAAGTATAACGTGCTGTGTGAATACATAAATCAAACAGAACGTGGTCC
 CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT
 ACACGTGGAGTCCCTTCGTCGCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAATCATCTCTGGTATGTTTTG
 CCCATATCTATTACCGTGTTCCTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
 CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTATGGAAATGAATTTGACAAA
 GATTCCTTTGTGCTGCTGAAAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGAT
 TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA
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 GGTATGCTTCGCATTGTGATGGAATTTTTTGTGACTCTGAAGAAAAACACGGAAGGTACTTCT
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCGGATAAAACAGTCATTGAATATGA
 ATATGATGTCAGAACCACTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGG
 AGGAGGTGTCACACAAGGAACATTATTGGAGTCGACGGCAGCGTTGGCAGTCTTGGCCCCG
 CAAACGTTACAGTACTCATACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGCCGAGGAAGAGCCATCGACGACCTGGTCGACTGGGATCCCC
 AAACGTCAGGCTGTGTATTCTTCGCTGTTCAGCTTCGACCAGGATTAGAGGGCTGCGAG
 CCTTCTGAGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
 TCCAGACAGGCCACCAGGAGAAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT
 TATATGTGCAGATGGAAACTGGATGCCAACACTTCCTTTTGCTTTTGTTCCTGTGCAAC
 AAGTGAGTCACCCCTTTGATCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT
 TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTCTCTATTCTCATAGCACGTGTGTGATTG
 GTTCATGCATGTAGGCTCTTTAACAATGATGGTGGGCTCTGGAGTCCAGGGGCTGGCCGGT
 GTTCTATGCAGAGAAAGCAGTCAATAAATGTTGCCAGACTGGGTGCAGAATTTATTTCAGG
 TGGGTG

FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRVFKELKLLTLCSSISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLFVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHANLILYIGNEFD
KRFFVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYEDVVRTTDICAGPEEQELSL
QEEVSTQGTLLSQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGECEPSEGDGLGEEGLLSRLYEAPDRPPGENETYLMQFMEEW
GLYVQMEN

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
TCTGCCATGGGGCTCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG
TGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA
GGCTTCTGCTGCGAGCCCGTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT
CCGCACTGCGCTGGTGGTGTCTGGGCGCCACGTCTTCTGAGTACTGCGGAGCCCCACCCAGCAGG
TGTTTGGCATCGATGCTCTCACCACGCACCCGACTACCACCCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTCTGGGCCCTGCAGTGGGGCTGCTGAGGCT
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGTGGAC
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGCAGGA
ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGAC
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCC
CCAGCCCGGCCCTGCTGGGACCACCAGGCCCCAGGAGAAGCCGCCTTGAGCCACAACCT
TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTACAGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAACCAGTAAATGTTAACTGACAAAAAAAAAAAAAAAAAAGAAA

FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPVGLRLPLGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLLTLMCTRSRSGDSHRRGFCSSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSFAVVAWIWDVVRSSPQPGPLPGTTRPPGEAA

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGGTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCTGACGCGCTGA
CGCCTGTCCCCGGCCCCGGC**ATG**AGCCGCTACCTGCTGCCGCTGTGCGCGCTGGGCACGGTAG
CAGGCGCCGCGGTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCCAGCAAGGCCACC
ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
GGAACTGGCCAGGAGAGGAGGCAACATCATCTGCGCTGCCGAGACATGGAGAAGTGTGAGG
CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCCACCTGGAC
TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACAGCAAAGATCATTGAAGAGGAGGAGCGAGT
GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT
TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTCTCTTGACAAAATTGCTGCTGGAC
AAGCTGAAAGCCTCAGCCCCCTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG
GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
GCCAGACCAAGCTCGCCCATCTGCTCTTCAACAGGAGACTGAGCCGGCGGCTGCAGAGGCTCT
GCTGTGACTGTCAACGCCTCCCTCACCCTGGCGTGGCCAGGACAGAGCTGGGCAGACAACGGG
CATCCATGGCTCCACCTTCTCCAGCACCACACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA
GCCCCGAGCTGGCCGCCAGCCAGCACATACTGGCCGTGGCGGAGGAAGTGGCGGATGTT
TCCGGAAGTACTTTCGATGGACTCAAACAGAAGGCCCGGCCCCGAGGCTGAGGATGAGGA
GGTGGCCCGAGGCTTTGGGCTGAAAGTGCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGA
GGGAGCAGCCCTCCCCAGTA**TA**ACCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG
ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCTTGGCACTACCTGAGCCGGGAGACCCAG
GACTGGCGGCCCGCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGCAGTGGACTGGC
CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG
AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC
TGTGCACTTGCAGGCCACGTGAGGAGAGCCAGCGGTGCTGTGCGGGAGGGTTCCAAGGTGC
TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGACCT
TGTGCATGCATGGTCCCTCTCTGAGCCTTGGTTTCTTACGAGTGAGATGCTCAGAATAACTG
CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
GGTGGTTTGTCTGAGGGCTTCTGTGCCAGAGCCCAGCCAGAGAGCAGGTGCAGGTGTCATCCC
GAGTTCTAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA
TTGGCTGGGACTCCCACCTTCCATCAATTCTCATGGTAGTCCAACCTGCAGACTCTCAAC
TTGCTCATTT

FIGURE 66

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERV DILINN
AGVMRCPHWTTEDGFEMQFGVNH LGHFLLTNLLLDK LKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAAYCQSKLAIVLFTKELSRRLQSGSVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC
 CAGCGTGGCGCGCGCCCTGGCGCCCGAGCGCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCAT
 GAGGATTCAACAACCCCTGTGGCTAACCCCTGCTGTGCATTTACTCTCATCAAACGCGCTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGAGAGCAAGG
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCGAGGTGTCTT
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTCTCTCA
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC
 ATTCATGGCTGGAGGAGGTGTCACTCTCTCCGAGGATCTTACGGAGAGTGGAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCGAGGAA
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTACAGCCAGATAATAAGAGG
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTTTGGCAGAGAGCCCCAACACGTGGTAGC
 TGAGGCTGTCACTCCAGAGGCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC
 TATGTCAGACCTGGGTTCCAGCCCACTCTCTACAGATCCCTAGCCTCTACTGTTCTTAT
 GAGACCAATCCAACGCCTACCTGCTGCTCCAGCCATCCGGAAGGAGGTCACTCCACCTGGA
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTCACTGCTGGTGGCATCAGGGGAGAAAGCATACAAGTGGAG
 TACCGCATCAGCAAAAGTGCTGGCTGAAGGACACTGTTGACCCAAAAGTGGTGACCTCAA
 CCACCGCATTTGCTGCCCTCAGGCGCTTGATGTCGGGCTCCCTATGCAGAGTATCTGCAGG
 TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTGACCATGCTACGTCACCAAGC
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCTGTGGTTAGGA
 ATGCAGCACTGTTTTGGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
 GCTGGCTGTCCCTGTCTGGTGGGAGATAAGTGGTGGCCAAACAGTGGATACATGAGTATGG
 ACAGGAATTCGCGAGACCCCTGCAGCTCCAGCCCTGAAGCA**TGA**ACTGTTGGCAGAGAGAAGC
 TGGTGGAGTCTCTGGCCTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCCTGGGAAGAAGGCCTTGTCACTTGTCTGTGCTCGCAATCAGAGGC
 AAGGGAGAGGTTGTTACCAAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCCTGAGAGGGAAGTTCTGG
 AGTTCAGATACTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTTCATCAGTGGGTC
 TTTTGGCACTTTGAACCTTGACCAGGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG
 GGGCTAGCCTGACTCCCAAGACTTAAAGACTTTCTCCCACTGCTCTGCTGCAGCCCCAAG
 CAGGAGGTGTCCTCCCTCCCAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTT
 TTTAAGTTGAAAACAACCTTTCTTTCTTTTGTATGATGGTTTTTAAACAGTCATTAAAA
 ATGTTTATAAAACAAA

FIGURE 68

MGPGARLAALLAVLAIGTGDPERAAAGDTFSALTSVARALAPERRLGLLLRRYLRGEEARL
 RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
 QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ
 VGKVAYDMGDYYHAI PWLEEAVSLFRGSYGWKTEDEASLEDALDHLAFAYFRAGNVSCALS
 LSREFLLYSPDNKRMAENVLYERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLGS
 QPTLYQIPSLYCSYETNSNAYLLQLPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
 RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAAYLQVVNYGIG
 GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSEAGGATAFIYANLSVPVVRNAALFWW
 NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTTAAAGTTCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG
 GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
 ACGAGCGTGGCTGAGGGACCGAGCCGAGAGCCCCGAGCCCCCGTAACCCGCGCGGGGAG
 CGCCAGGATGCCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
 TGGTCAAGTTTTACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGGCCCTGGTCCT
 GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTGAAAGTGCCCTCC
 TGGTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCATGTTTATGCTCTCCTTCATTGGT
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGAT
 CTGCTCATCATGGAGCTCATTGGTGGCGTGGTGGCTTGACCTTCCGGAACCAGACCATTG
 ACTTCTGAACGACAACATTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA
 AACATCATGGACTTTGTTGAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
 GAGCAAGAATCAGTACCACGACTGCAGTGCCCTGGACCCTGGCCTGTGGGTTGCCCTACA
 CCTGTGTCATCAGGAACACGACAGAAGTTGTCAACACCATTGTGTGGCTACAAAATATCGAC
 AAGGAGCGTTTCAGTGTGCAAGGATGTATCTACGTGCGGGGCTGCACCAACGCCGTGATCAT
 CTGGTTCAATGGACAACCTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
 TCCTGGGGGTGCTGCTGACGTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC
 TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG
 ATGCTGCTTGTGCTACCCCAATTAGGGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
 TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGCTGTGTGTAGGTCCCACGGCCTCTGCCTC
 CCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGCTTCCCCGAGGCAGCTCTGGAATCTGT
 GCCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA
 GAGCTGAGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCCCTTGGCGGTGGTATTCAA
 GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGAGGAGGGAAGG
 GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCCAGGTGGC
 CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCTTGAGCCTA
 GTTTTTTTTTACGTGATTTTTGTAACATTCAATTTTTTGTACAGATAACAGGAGTTTCTGAC
 TAATCAAAGCTGGTATTTCCCGCATGTCTTATTCTTGCCCTTCCCCAACCCAGTTTGTAA
 TCAAACAATAAAAAACATGTTTGTGTTTTTAAAAA

FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIIAEVERQKYKTLES AFLAP
AIIILLGVVMFMVVSFIGVLASLRDNLVLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL
NDNIRRGIIENYYDDLDKFNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVIIWFMNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACCTTGCTGCCCTCTGA
 CACCTGGGAAGATGCGCCGGCCCGTGGACCTTCACCCCTTCTCTGTGGTTTGCTGGCAGCCACC
 TTGATCCAAGCCACCCTCAGTCCCCTGCACTGCACTTCTCATCCTCGGCCCAAAGTCATCAAAGA
 AAAGTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGTGCCGCTGC
 TCAGTGCCATGCGGGAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC
 GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACACGCCCTTGGTCAAGACCATCGTGGAGTTCACATGACGACTGAGGCCAAGCCACCATC
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCTCAGTGACTGTGCCACCAGCCA
 TGGGAGCCTGCGCATCCAACCTGCTGTATAAGCTCTCCTTCTGGTGAACGCCTTAGCTAAGC
 AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG
 ATCGAGGCTTCCCTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATTTC
 CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTTC
 AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC
 TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTAGCCTCATCGTGAGTCA
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCCAGAAGAATTATGGTCTGTGG
 ACTCTGTGCTTCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCCACTGATCGTGCTGGAAGTGTTCCTCCCA
 GTGAAGCCCTCCGCCCTTGTTCACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC
 ACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
 GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
 ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCAGTGTCATTGGTG
 AAGGCCTTGGGATTGAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCC
 AGCCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCCAGTGAAGACTTGATGGCAGCCATCAG
 GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
 CAATAACACTTGCCCTGTGAAAAA

FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIEKLTQELKDNATSILOQLPLLSAM
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLFEFDLLYPAIKGDITQLYL
GAKLLDSQGKVKWFNNASALTMPTLDNIPFSLIVSQDVVKAAVAVALSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPFEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGIEASSEAQFYTKGQDLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIHSIL
LPNQNGKLRSQVPSLVKALGFEESSSLTKDALVLT PASLWKPSSFPVSQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAACATGGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG
 CTCATCGTTTGCAGACGTTCCCTCAGCCTCTGCCCAAAGAAAGGAGATGGTGTTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAGACCTGTAATAAGAATGAATGGAGACA
 AGTTC CGTCGCTTGTGAAAGCCCCACCAGAGAATTACTCGGTTATCGTCATGTTCACTGCT
 CTCCAACTGCATAGACAGTGTGTCGTTTGAAGCAAGCTGATGAAGAATCCAGATCCTGGC
 AAACCTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTGCCATGGTGGATTTTG
 ATGAAGGCTCTGATGTTATTTTCAGATGCTAAACATGAATTCAGCTCCAACCTTTCATCAACTTT
 CCTGCAAAAGGGAACCCAAACGGGGTGATACATATGAGTTACAGTTCGGGGTCTTTTCAGC
 TGAGCAGATTGCCCGTGGATCGCCGACAGAAGCTGATGTCAATATTAGAGTGATTAGACCCC
 CAAATTATGCTGGTCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT
 CTTTCAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTGCAGCTTTGTG
 TTTTGTGCTTGCTATGACATCTGGTCAAAATGTGAACCATATAAGAGGACCACCATATGCC
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCAGTTTGTG
 GCTGAAACACACATTGTTCTTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGCTTTTATG
 TGAAGCTGTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG
 GACTTGTGTATTATTCTTCAGTTGGATGCTCTCTATTTTATAGATCTAAATATCATGGCTAC
 CCATACAGCTTTCTGATGAGTTAAAGTCCAGAGATATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAATCGTGTGTGTTGAAAAGAAGATGCAACTTGTATATTTGTATTAC
 CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCAAATCTGAGGTATTGAAAATAATTATCCTCTTAACCTTCTCTT
 CCCAGTGAAGTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAATTTGTA
 CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACACTACTTAGTTAACTTGGTCACTGTAT
 TTTATATTGCCTTATCCAAAGATGGGGAAGTAAGTCTGACAGGTGTTCCACATATGCC
 TGTTACAGATAACTACATTAGGAATTCATTCTAGCTTCTTCACTCTTTGTGTGGATGTGTAT
 ACTTTACGCATCTTCTCTTTGAGTAGAGAAATTATGTGTGTCATGTGGTCTTCTGAAAATG
 GAACACCATTCTTCAGAGCACAGCTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCTCCTT
 GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTTAACTACCTTGTATTAGAAA
 GATTTTCAGATTCACTCATCTCCTTAGTTTTCTTTAAGGTGACCCATCTGTGATAAAAAA
 TAGCTTAGTGCTAAAAATCAGTGTAACCTATACATGGCCTAAAAATGTTTCAAAATTAGAGT
 TTGTCACCTTATCCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CAGGCGCAGTGACTTACCGCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC
 GAGGTGAGGAGTTCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT
 AAAAATAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCAGCTACACAGGAGGCTGAGGCAC
 GAGAATCACTTGAATCAGGAGATGGAGGTTTCAGTGAGCCGAGATCAGGCCACTGCACTCC
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMEWTKRPFVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFFINFPKAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

FIGURE 76

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFDGRLLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSKGHSISNRVEAWTRDVAFLLRQEGRPVNLIRNRTKVRVMERDQNTDKAVNW
LRKEAINYTEPFVIYLGNLPHYPSPSSGENFGSSFTHTSLYWLEKVSHTDAIKIPKWSPLS
EMHPVDYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY
SSDHGELAMEHRQFYKMSMYEASAHVPLMMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS
ILPQLFDLSSDPDELTVNAVVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
 GCCTCTCTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
 GGTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAG
 CAGTTGGCTTCTCCAAGGGCTCTGGATGGAATGTGCCACACACAGCACAGGCATCAGCCAG
 TGTGACATCTATAGCACCTTCTGGGCTGCCCGCTGACATCCAGGCTGCCAGGCCATGAT
 GGTGACATCCAGTGCAATCTCCTCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
 CAGTCTTCTGCCAGGAATCCCAGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTC
 ATCCTTGGAGGCCTCCTGGGATTCATTCTGTGCTGGAATCTTCATGGGATCCTACGGGA
 CTTCTACTCACCCTGGTGCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG
 GCATTATTTCTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCC
 CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCCAACCTCTTGCCACAAGGAGCTC
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGT
 ATGTG**TGA**AGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC
 CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAACCCACTAATCACATCCCACTG
 ACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTTGCTGG
 GGATGGGAAGGAGAAGCAGTGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
 TCCAAGAAACTGATTGGCCCTGGAACCTCCATCCCCTCTGTGTTATGACTCCACAGTGTCC
 AGACTAATTTGTGCATGAACTGAAATAAAACCATCTACGGTATCCAGGGAACAGAAAGCAG
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAAATA

FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYYLGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPIVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
```

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

FMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCC**ATG**GTGCCCAGAATCTTCGCTCCTGC
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCCCTTTGGCCTCACAAACGATTTTGTG
TGAAGCTGAAGGTTCAGGGTGAATTCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTTCCCT**TGA**GAAAGACATAGAAAGAAAATCAACTTTCATAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

FIGURE 80

MVPRI FAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTNDFFVKLVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

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FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCCTGCAGCACTGTT
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA
GTCTGCTTTGAGCAGTGTGCCCCTGACCTTCATGGTGAAGCTGATAAACCAGAAGTGCGA
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGCTTAATGGAACATCAGGGGAA
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACTTCATT
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCCTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCCTCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCCCTTACCCT
TCTGTGAGATTTCCATCATCTCAAGTTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTTATGTACTTTATAAATGAAAA

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCGACGCGCTCACTCGCTCGCACTCAG
 TCGCGGGAGGGCTTCCCCGCGCCGGCCGCTCCCGCCCGCTCCCGGACACCAGAAGTTCTCTCT
 GCGCGTCCGACGGGCGAC**CATG**GGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA
 TCCCTGCTCTTCGCTCTTCTCCTGGCTGCGTCCCTAGGTCGGTGGCAGCCTTCAAGTTCGC
 CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCAGAACGTACCCCTACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGGCAGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
 GCGAGGTGCAGACCTGCTCAGAGCGCCGGCCATCCGCAACCTCACGTTCAGGACCTTCA
 CCTGCACCATGGAGGCCACCAAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCTGTCTG
 GATAGCGGCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACCTCGGAGCACAGGGT
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAGATGCACCATCCAACCTGTGTGGTGT
 ACCCATCTCCTCCCAGGATAGTGAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC
 CTCGAACCGCGGTGCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAAACC
 CCGGCTTTGAAGCCTCACCACTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGGCCAGCAC
 CCCCCTGTCTCCTCCAGGCCCGGAGACGTCTTCTTCCCATCCCTGGACCCCTGTCCCTGACT
 CTCCAAACCTTTGAGGTCACT**TAG**CCCAGCTGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG
 GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCTCCTTGGCTCGGCCCTGGTTC
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCAGAAGCCAGCCCTCAACCCCTC
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTTGGGGTGTGAG
 ATTCTCCCTTAGAGACCTGAAATTACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
 GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA
 GCATCAGTGGGACAAGATGGACACTGGGGCACCCCTCCAGGCACCAGACACAGGGCACGGTG
 GAGAGACTTCTCCCCGTGGCCGCCTTGGCTCCCCGTTTGGCCCGAGGCTGCTCTTCTGTG
 AGACTTCCTCTTGTACCACAGTGGCTCTGGGGCCAGGCTGCCTGCCCACTGGCCATCGCC
 ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCGAAACGGGAAGTAC
 ATATTGGGGCATGGTGGCCTCCGTGAGCAAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG
 ATGTTGCCCCACCCACTGGAGATGGTGTCTGAGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCTACTCCCACTGCTCAGCGCGGGCC
 ATTGAAGGGTGCCACACAATGTCTTGTCCACCTGGGACACTTCTGAGTATGAAGCGGGAT
 GCTATTAAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLFLFALAASLGPVAAFVKVATPYSLYVCPEGQNVTLTCRLLGPVVK
GHDVTFYKTYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVCVYPSSSQ
DSENITAAALATGACIVGILCLPLILLLVYKQQAASNRRQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT
 TTCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCTGCCCCTCC
 TTTCTGCCCACCGCTGCTTCTTGCCCTTCTCCGACCCGCTCTAGCAGCAGACCTCCTGG
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCCTCCCGA
 CTCGCTCCCGGACCAGCGGCTGACCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCTCT
 TCCTCCTTGTCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCACGCTCGAGCCCGCC
 AGACATGTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACT
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT
 TGTTACCGCTCCACTGTCCGCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCC
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCTCTCC
 CGCTGCCCAACCAAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC
 AACCTGCCCGAACCAGGCTGCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT
 GCAAAGATGAGGCAAGTGAACAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG
 AGACATCCTCAGGATCCATGTTCAGTGATGCTGGGAGAAAGAGAGGGCCGGGCACCCAGC
 CCCCCTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGGCACCTTCAGACCCAAGGGAGCAG
 GCAGCACAACCTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG
 AAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCTTGCCTTG
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
 ACCCTGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCCAGAGGACAAA
 GCAGACCCTGGCCACAGTGAATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCTT
 CGTCCACACATCGGTATCCCCAAGCCAGACAACCTGCGTCGCTTTGCGCTGGAACACGAGG
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTTCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCAC
 GAAGTCACTGGAACGTCTTCCTAGCCCAGACCCTGGAGCTGAAGTCAAGGCACGGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT
 ATTATATATTAATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 86

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSLLGLALLWFPLDSHARAPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQFPVTEPQCCPKCPEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFP SRLPNQCVLCSCCTEGQIYCGLTTCPEPGCPAPLPLPDSCCCACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGPPTAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGLPCILCTCEDGRQDCQRVTCPT EYPCRHPKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL V
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSPDPG
AEGHGQSRQSDQDITKT

```

Signal peptide:

amino acids 1-25

FIGURE 88

MDSL RKMLISVAM LGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA
TLQEAATTQENVAWRKNWMMVGEGGASGRSP

Signal peptide:

amino acids 1-18

FIGURE 89

FIGURE 90

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLILFLLSWGPLQGQQHHLVEYMERRLAALAEERLAQCQDQSSRHAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETONPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDGTYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVRVFPWPVGTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCALDPQTLDTQEQ
QWDTPCPRENAEAAFVICGTLVYVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV
```

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCAT
 CCGTCACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGG
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGCCAGGTGTTT
 GGGCCAGACAAGCCTGTCCAGGCCCTGGTGGGGAGGACGCAGCATTCTCCTGTTTCTCTGTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGAAAAACATTAC
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGCTTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCTCTCATTTCCATCACGGGATATGTT
 GATAGAGACATCCAGCTACTCTGTCACTCCTCGGGCTGGTTCCCCGGGCCACAGCGAAGTG
 GAAAGGTCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTTTGATGTGGAGATCTCTTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTCGA
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
 GCATTGTTGGACTGAAGATTTTCTCTCCAAATTCAGTGGAATAATCCAGGCGGAAGTGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCAGTGAGGTTGAC
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAAGTGAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTTCCAAGCAGGGAACATTACTGGGAGGTGGACGGAGGACAAATAAAGGTG
 GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGTCTTCTGGACTATGAGTG
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCTGCATGTCGGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTATAATGAGCAAAATGGAAGTCCC
 ATAGTCATCTGCCAGTCAACCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC
 AATCCAGAGACAAGCAACAGTGAGTCTCCTCACAGGCAACACGCCCTTCTCTCCCAGGG
 GTGAAATGTAGGATGAATCACATCCCACATTCTCTTTAGGGATATTAAGGTCTCTCTCCCA
 GATCCAAAGTCCCGCAGCAGCCGCGCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTCTAGTGTGCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACTCTCAGGTGAAGAACCG
 TCAGGAATCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA
 AAAAAA

FIGURE 92

MALMLSLVLSELLKLGSGQWQVFGPDKPVQALVGEDAAAFSCFLSPKTNAEAMEVRRFFRGQFSS
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGDLSTDSRTNRDMH
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELDWRRKHGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQSFAQGKHYWEVDGGHNRWRVGVCRDDVDRRKEYVTLS
PDHGYWVLRNLNGEHLVFTLNPRFISVFPRTPTTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQSESEKEASWQRASAIPESTNSSESSQATTFFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGC GCCCGGTGGCGGTGGCGGCGGCGGTGCGGAGGCTTCCTTGGTCGGATTGCA
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC
 CATGAGGAGCCTGCCGAGCCTGGGCGGCGCTCGCCCTGTTGTGCTCGCGCCGCGCCGCGCCG
 CCGTCGCGCTCAGCCGCTCGGCGGGGAATGTCACCGGTGGCGGCGGGCGCCGCGGGCGAGGTG
 GACGCGTCGCGCGGCCCCGGGTTCGCGGGCGAGCCAGCCACCCTTCCTAGGGCGACGGC
 TCCCACGGCCCCAGGCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCCGACCCTGGCTG
 CGACTTCTCCAGCCAGTCCCGGAGACCACCCTCTTTGGGCGACTGCTGGACCTCTTCC
 ACCACCTTTCAGGCGCGCTCGGCCCTCGCGGACCACCCTCCGGCGCGGGAACGCACCTTC
 GACCACCTCTCAGGCGCCGACCAGACCCGCGCCGACCACCTTTCGACGACCACTGGCCCCG
 CGCCGACCACCCTGTAGCGACCACCGTACCGGCGCCACGACTCCCCGGACCCCGACCCCG
 GATCTCCCCAGCAGCAACAGCAGCGTCTCTCCCGACCCACCTGCCACCGAGGCCCTC
 TTCGCTCTCTCAGAGTATGTATGTAAGTCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACCAGGGCAGTGTGAGTGTGCGGCCAGGTATCAGGGGCTTCACTGTGAAACC
 TGCAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGCAACAGGTAAGCAACAGAGGGTGGAACTGAAGTTTAT
 TTATTTTAGCAAGGGAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG
 GAGGATGAGGGTCATAGATTTACAAAATATTTATATACCTTTTACTCTTATATGT
 TATATTTAATGTGAGGATTTAAAAACATCTAATTTACTGATTTAGTCTCTCAAAAGCACTAG
 AGTCGCAATTTTCTCTGGGATAATTTCTGTAATTTTCATGGGAAAAAATTATTGAAGAT
 AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT
 ATGTTTATTAATATACCATTTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTCTCTCTA
 ATCAAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCATTTTA
 TTTAACTAGTGGTAAGTAGACTGGTTTACTCTATTTACCAGTACATTTTGGAGCAAAAAG
 TAGATTAAGCAGGAATATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGGA
 ATAATGTACTGTTATCTAAGCAATTTGCCCTGTACTGCACTGAAAGTAATTTCTTTGACCT
 TATGTGAGGCACTTGGCTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAT
 AATGAAAAAATAATGACAGGTTATACTCAGTGTAACTGGGTATAACCCAAGATCTGCTGC
 CACTTACGAGCTGTGTTCTTGGGCAAGTAATTTCTTCTACTGAGCTTGTTCCTCTCAAG
 GTTGTGTGAAGATTAATGAGTTGATATATATAAAATGCCATGACATGTCACTCAATAAA
 TTCTGGTTTGTGTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTAAAGA
 ACTTTTAGCTCCTTGACAAAGAAGTGCTTTATACTTTAGCACTAAATATTTTAAATGCTTTA
 TAAATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTAAAAATGTAGAAG
 AGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGCGGGTGGAT
 CACTTGAGGCCAGAGTTCTAGATGAGCTGGCCAGCACAGTGAACCCCGTCTCTACTAAA
 AATACAAACAAATAGGCTGGCGGTGGGCACACACCTGTAGTCCAGCTACTCGGAGGCT
 GAGGCAGGAGAATCGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGGCCACT
 GCACCTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLSLGGGLALLCCAAAAAASAGNVTTGGGAAGQVDASPGPGLRGEPSPHPFRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPWATAGPSSTTFQAPLGPSPTTPPAAERTS
TTSQAPTREAPTTLSTTTGPAPTTVPATTVPAPTTPRTPTPDLPSSSSSSVLETPPATEAPS
SPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGGCATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGGTGGTGGTGACCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTACCAAGTGGAGCAGGAGC
CTGGGCTTCTGTGCACAGTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT
CCTTCTGTGAGTGTGCGTCCCCAGTAGGGATGGCGCCCACAGGGTCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCCAGCACCAGCTCAGAATAAAGCGATT
CACAGCA

FIGURE 96

MGGLLLAAFLALVSVPRQA¹AVWLGR²LDPEQL³LG⁴PWYVLAVASREKGFAMEKDMKNVVG⁵VVVT
LTPENNLRTLSSQHGLGGCDQ⁶SVMDLIK⁷RNSG⁸WVFENPSIGVLELWVLATNFRDYAIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTK⁹WSRSLGFLSQ

Signal peptide:

amino acids 1-20

FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGAC**ATG**CTGCTGCTGCTGCTGCC
 CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGCAGGAAGGCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
 GGTGATTACCTGGCCAGTAGTTCATGGCTACTGGTTCGGGAAGGGGCCAATACAGA
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCTGAGCATCAGAGATGCCAGA
 AGAAGTGATGCGGGGAGATACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCCAG
 GCACCTGGAGTCCGGCTGCCCCAGAATCTGACCTGCTCTGTGCCCTGGGGCTGTGAGCAG
 GGGACACCCCTATGATCTCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
 CCGCTCCTCGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
 AGGTGACCTTCCCTGGGGCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC
 CCGCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
 AAATGGCTCATCTCTGTCACTCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAATTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGCCTGACCCTGTGCCCC
 TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA
 ATTACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTGGGGGAGCTGGAGCCACAGCCCTG
 GTCTTCTGTCTTCTGCGTCATCTTCTGTGTAGTGAGGTCTGCAGGAAGAATCGGCAAG
 GCCAGCAGCGGGCTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTAGCCT
 CTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCAGACCAGCCTCCCCAGCT
 TCTGCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
 ACAGAT**GGA**AACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA
 GAAGTCAGAGGCTGATTCTTGTAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTATTTTTTAACTAAAGACAGACAAATTCCTA

FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTTPMISWIGTSVS
PLDPSTTRSSVLTLPQPQDHGTS LTCQVTFPGASVTNKTVHLNVSYPQNLMTVVFQGDG
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVS LQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
CRKKSARPAAGVGDTGIEDANAVRG SASQGPLETPWAEDSPPDQPPPASARSSVGEGELQYA
SLSFQMVKPWD SRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAG**ATGA**AAGACCCTGTTCCCTG
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCGGAGGACAGGAGGCCCAGGA
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACT
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCCTGCTCCACATGGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTTCACGCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC**TAGG**
CAGCCCCCGGGTCTGCACCTCCAGAGCCACCTACCACCAGACACAGAGCCCGGACCACCT
GGACCTACCCTCCAGCCATGACCCTTCCTGCTCCACCCACCTGACTCCAAATAAAGTCCT
TTTCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 100

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALLEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

Important features:**Signal peptide:**

amino acids 1-17

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
 AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA
 TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTTCGAG
 TGCAAGCCTCACTCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGG
 GCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA
 TAGTTACCTGGGGCAGCACAACTCCAGAAGGAGGGGCTGTGAGCAGACCCGGACAGCC
 ACTGAGTCCTTCCCCCACCCTGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
 CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
 TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC
 AGCCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCA
 GAAGTGTGAGAACGCCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG
 AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCACTCTCTT
 CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC
 GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA
 CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTGTTGGTTCTGTTCACCTCTGTAAAT
 AAGAAACCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG
 CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTTGCCTT
 GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCA
 AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTGCTAAATGAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIIHQKCNAYPGNITDTM
VCASVQEGGKDCSQGDSGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWQIETMKNN

```

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTCTGCTGGAGCCGATGCCAAAAACCATGCATTTCTTATTAGATTTCATTGTTT
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACC GAAGAA
GTGAAAATAGAAGTTTTGCATCGTCCAGAAAAGTCTCTAAGACAAGCAAGAAGGGAGACCT
ACTAAATGCCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCCAAATGGTTTGTCTTGGTGTGGGCAAGTCATAAAAGGCCATA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT
TGCATACGGAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG
AGATTGAACCTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTAAGA
AGAATGACCATGATGGTGATGGCTTCATTTCTCCAAGGAATACAATGTATACCAACACGAT
GAACTATAGCATATTTGTATTCTACTTTTTTTTTTTAGCTATTACTGTACTTTATGTATA
AAACAAAGTCACTTTTCTCCAAGTTGTATTGTCTATTTTCCCTATGAGAAGATATTTTGA
TCTCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTGCAAACTTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLVGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLNNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTMCPEGKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDDHGDGFISPKYENVYQHDEL

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Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAACAAAACCTTCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTCACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCCGTGTCTACTAAAAATACAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTTCTTGTTTCATTTTCGCGACTGCCCTCTCAGTGTTTCTGGGATCCCCTCCCAAATAA
AGTACTTATATTCTC

FIGURE 106

MQGPLLLLPGLCFLLSLFGAVTQTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL
ETCNARHGG SRL

Signal peptide:

amino acids 1-18

FIGURE 107

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC
 AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACCATGG
 GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
 TTCAATGGCACTGAGTGTGGCGTAACCTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
 CAGCCTGCGCTGCGGGGGTGCTTATTGACCACAGGTGGGTCTTCACAGCGGCTCACTGCA
 GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
 CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCC GGCTACCTGGGAGCCTCGACGAGCCA
 CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC
 CCCTGCCCTTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC
 ATCACCAACCCACCGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT
 CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG
 GCGGCGTCCCGGGGCAGGATGCCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA
 GTCCTTCAAGGTCTGGTGCTCTGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
 AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGAC
 CTGTTTCTCCACCTCCACCCCAACCCCTTAACCTTGGGTACCCCTCTGGCCCTCAGAGCACC
 AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACCTTCTTGGAACCTT
 TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGTGAGAGAAGTGTGCAATAGTCTGGA
 ATAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

FIGURE 108

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLPVRVTSSV
QPLPLPNDCATAGTECHVSGWGITNHPNPFDDLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSGVGPCGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
 CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATG**TCGGGCGAGCTCAGCA
 ACAGGTTCCAAGGAGGGAAGGCGTTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC
 GAGATCAACCGGGAGTTTCTGTGTACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA
 GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC
 TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
 AAGATGATCTCAGAGGTGACAGGAGGGGTCACTGACACTATATCCTACCGAGACTTTGTGAA
 CATGATGCTGGGGAACGGTTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCCTCCAGAGAGAGACATTGCTAGCCTGCC**CTGA**
 GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
 CTTGACACACTGTGATCTCTCTCTCTCATTGTTTGGTCATTGAGGGTTTGTGTGTTT
 TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTCGGGGAATCC
 TGAGCCTTGGGTCCCTCCCTCTCTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG
 ATATCAAACCAAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
 CTCACTTGGAGGAACAGCACTCTCCATCCTTTAGAAAGTCTCCAAGCCAAGTTCAGGCTC
 ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
 CTGCAGGGCCTCTTTCGGGTTTCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTCAACC
 AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCACACCTCTTCT
 CATCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG
 TACCAGAAGGAACCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG
 CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGAGGCAGAAAGTGAAGGCCTG
 GGGTTTGGGGGAAAGGTCACTCAGTGTCTTCCACCTTTTAGGGAGGATACTGAGGGGAC
 CAGGATGGGAGAAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
 CTGAGAAATACAAGTTGCTTGTCTGACCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN
NEGEIDLMSLKRMMKELGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRS AVLKLV
MFEGKANESSPKPVGPPPERDIASLP

FIGURE 111A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA
 GGAGCGGGGCCCTGCACACATGCGCCCCGGGTGGGCAGGGGTGGCGCCCGCGCTGCGCGCC
 CGCCTGGGCTGGCCTTGGGCTGGCGAGCGTCTTGAGTGGCGCTCCAGCCCTCGCCTGCCC
 CACCAAGTGTAACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCCTCCGCGGGTTC
 CTCGGGGATCCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC
 ACCAAGATTGGATCTCGCTGGGCTCAAGAACCCTCCGAGTCTTGATCTGGGAAGACAACCGGT
 CAGCGTCATCGAGAGAGGCGCCTTCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA
 AGAATAAGCTGCAAGTCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA
 GATTTGAGTGAACACCATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCAGTGT
 GAAGAACCTGCAACTGGACAACAACCATCAGCTGCATTGAAGATGGAGCCTTCGAGCGCG
 TGCGCGATTGGAGATCCTTACCCTCAACAACAACAACATCGCATCCTGGTCAACGAG
 TTCAACCACATGCCGAAGATCCGAACCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG
 CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTACACACTCT
 GCATGGCTCCTGTGCATTGAGGGGCTTCAACGTGGCGGATGTGCGAGAAGAAGGATACGTG
 TGCCCGACCCCCCACTCGGAGCCCCCATCCTGCAATGCCAACTCCATCTCCTGCCCTTCGCC
 CTGCACTGCGAGCAATAACATCTGTGACTGTGAGGAAAGGGCTTGATGGAGATTCTGCCA
 AACTTCCGGAGGGCATCGTCGAAATACGCTAGAACAGAACTCCATCAAAGCCATCCCTGCA
 GGAGCGCTTCAACCAGCTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
 TATTCTCCAGATTGCCCTTCAGGGGCTGAAATCACTACATCGATCCTGTATGGGAAACA
 AGATCACCAGATTTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC
 AATGCCAACAAAGATCAACTGCTGCGGGTGAAACACGTTTCAGGACCTGCAGAACCTCAACT
 GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCTCTGCACT
 CCATCCAGACACTCCACTTAGCCCAAAACCCATTGTGTGCGAGCTGCCACTTGAATGGGTG
 GCCGACTACCTCCAGGACAACCCCATCGAGACAGCGGGGCGCCTGCAGACGCCCGCGCG
 ACTCGCCAAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG
 ATTACCGCAGCAGGTTTCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCGGAGAAGTGTGCG
 TGTGAGGGCAGGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCACTCCAAGCCACCTCCC
 TGAATATGTCACCGACCTGCGACTGAATGACAATGAGGTATCTGTCTTGAGGGCCACTGGCA
 TCTTCAAGAAGTTGCCCAACCTGCGGAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
 CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACAGCT
 GGAGACCGTGCACGGGCGCGTGTTCGCTGGCCTCAGTGGCCTCAAACCTTGATGCTGAGGA
 TTAACCTGATCAGCTGTGTGAGTAATGACACCTTTGCCGCGCTGAGTTCCGTGAGACTGCTG
 TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTACCACGCTTGTCTCCCT
 GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA
 AGTGGTTGAGGAAGAGCGGATCGTCAGTGGGAACCTAGGTGGCAAGCCATTTTTCTCCT
 AAGGAGATTTCCATCCAGGATGTGGCCATCCAGGACTTCACTGTGATGGCAACGAGGAGAG
 TAGCTGCCAGCTGAGCCGCGCTGCCCGAGCAGTGACCTGTATGGAGACAGTGGTGGCAT
 GCAGCAACAAGGGGCTCCGCGCCCTCCCGCAGGCGATGCCAAGGATGTGACCGAGCTGTAC
 CTGGAAGGAAACACCTTAACAGCCGTGCCAGAGAGCTGTCCGCGCTCCGACACCTGACGCT
 TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGCTCT
 ACCTCTCCACTCTGATCTGAGCTACAACCGGCTGAGGTGCATCCCGCTCCAGCCCTTCAAC
 GGGCTGGCGTCCCTGCGAGTGCTAACCCCTCCATGGCAATGACATTTCCAGCGTTCTTGAAGG
 CTCTTTCAACGACCTCAGATCTCTTTCCATCTGGCGCTGGGAACCAACCACTCCACTGTG
 ACTGCACTCTTCGGTGGCTGTGCGAGTGGGTGAAGGCGGGGTACAAAGGACCTTGGCATCGCC
 CGCTGCGAGTAGCCCTGAGCCATGGCTGACAGGCTCCTGCTCAACACCCCAACCCACCGCTT
 CCAGTGCAAGGGCCATGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAGCG
 CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGACCGCTGTGCTTGGCC

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FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACCTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCCGTGCCCTC
 TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCCAA
 AACAAATGCCACCTGCGTGGACGGGATCAACAACACTAGCTGTGTATCTGTCCGCCTAACTACAC
 AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCCTGAGCTGAACCTCTGTGAGCATG
 AGGCCAAGTGCATCCCCCTGGACAAAGGATTAGCTGCGAGTGTGTCCCTGGCTACAGCGGG
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGTGCCGCCACGGGGCCAGTG
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCCCTCTGTG
 AACACCCCCACCCATGGTCCTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCAGAAC
 GGGGCCCAGTGATCGTGGTGACGAGGAGCCACCTGCCGCTGCCACCAGGCTTCGCCGG
 CCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAAGACTCCTACGTGGAACCTGG
 CCTCCGCCAAGTCCGACCCAGGCCAACATCTCCCTGCGAGGTGGCCACTGACAAGGACAAC
 GGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGT
 GCGGCTGGTCTATGACAGCCTGAGTTCCTCCCAACCACAGTGTACAGTGTGGAGACAGTGA
 ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCTGAACCTAGTAGTG
 GACAAAGGAACTCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG
 CCCCCCTTACCTTGAGGGCATCCCCACCTCCACCGGCCCTCTCCGCTTGCGCCAGGGCACGG
 ACCGGCCTTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG
 GACTTCAAGGCCCTCCACCACAGTCCCTGGGGTGTCAACAGGCTGCAAGTCTGCACCGT
 GTGCAAGCAGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG
 GCTGGACCGGCCCACTCTGCGACCAAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC
 CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG
 GGACTTGTGTGACAACAAGAAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCAACATG
 GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC
 GAGCACTGCCAACAAAGAGAATCCGTGCCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA
 GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTGCTGGGGGT
 GTGGGCCCAAGTGCTGCCAGCCCCCGCAGCAAGCGGCGGAAATACGCTCTTCCAGTGACG
 GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTC
 CTAAGCCCCCTGCCCGCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC
 ATGTGGGACCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAGAAGA
 AGAGAATATTAAGTATATTGTAAATAAACAATAAATAAGAACTAAAAAAAAAAAAAAAAAAAA
 AAAAA

FIGURE 112

MAPGWAGVGA AVRARLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
 AERLDLRNNITRITKMFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNKNKLQVL
 PELLFQSTPKLTRLDLSENQIQGIPRKA FRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNISRI LVSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL
 RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAIPAGAFQYQKLRIDISKNIQISDIAPDAFQGLKSLTSLVLVYGNKITEIAK
 GLFDGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTI SKGLFAPLQSIQTLHL
 AQNPVFCDCHLKWLDYLDQNPDIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS
 SECFMDLVCPEKCRCEGTIVDCSNQKLVRI PSHLPEYVTDLRLNDNEVSVLEATGIFKKLPN
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV
 SNTDTFAGLSSVRLLSLYDNRRITITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLRRR
 IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGRL
 ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLLTILDSNNSISMLTNYTFSNMHSLSTLIL
 SYNRLRCIPVHAFNGLRSLRVITLHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCLRWL
 SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHRFAQCKGPDVINIVAKCNACLSSPCKNNGT
 CTQDPVELYRCACPYSYKGKDVTPINTCIQNPCQHGGTCHLSDSHKDGFSCSCLGFEGQR
 CEINPDDEDNDCENNATCVDGINNYVICPPNYTGELCDEVIDHCVP EILNCQHEAKCIP
 DKGFSCECVPGYSGKLCETDNDCCVAHKCRHGAQCVDITINGYTCTCPQGFSGPFCEHPPMV
 LLQTSPCDQYECQNGAQCI VVQQEPTCRCPPGFAGPRCEKLI TVNFVGKDSYVELASAKVRP
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSPPPTTVYSVETVNDGQFHS
 VELVTNLNQLNLNVDDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
 HGCIEHVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVECECRPGWTGPLC
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDKNDSANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEHCQQENPLCGQVVREVIRROKGYASCATASKVPIMECRGGCGPQCCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCA
GACTCAACTGAGAACTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT
CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCTCATTTGGCTGCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAAGTGGCAAAAATATCTCGAGGGCTGGCCTG
GACAATTACTGGGGCTTCAGCCTTGGAAGTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGTCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAAACAACCACTGCCATGTGCGCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGAAAAAAGGCTGTGAGGTTTCCTAAACTGGAAGTGGACCCAGGATGCTTTGCAGCAAC
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCTCCCAATA
TTCCTTCTCAAACCTGGAGAGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGI FQINSFAWCRRGKLENNHCHVACSALITDDLTDALICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

FIGURE 115

CAGGCCATTTGCATCCCACTGTCTTGTGTTCGGAGCCAGGCCACACCGTCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCCTATTAACCTTGTACATGGCTCCC
 CATTGGTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCACTGTTT
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC
 CAAGAGAGATTCTTTTCTAAACGACTATACAGGCCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTACAGCTGCTGTTTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCTCTATCCATCTCTAAATGTACCAG
 CTTTGACTCAGTTGTTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAA
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCC
 CTCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCCACTGTCATTGCTGTTAATTCGGGTGGACCCCTGGAGT
 CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCCTTCTCAGAAGCA
 ATAGAAAAGTTCATCCGTGAACCTTCCTTAAAAGCCACCATTGGGCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAAATTTCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC
 TGCTGGTAT**TAA**TCAGATTGTTTTAAGATCTCCATTAATGTCACTTTTATGGATTGTAGACC
 CAGTTTTGAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTAAAAAATAAA
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA
 AACCATGTCTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
 TCATTCCATGTTCAGCAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA
 TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTCATAGTTAAGTGTGTATCATTTATCAA
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCACAGATTCAAT
 CCACCGAAGTGTTCACTGTCACTGTGTAGGGAATTTTGTGTTGCTGTCTTTGCCTGGATC
 CATAGCGAGAGTGCTCTGTATTTTTTTAAGATAATTTGTATTTTGCACACTGAGATATAA
 TAAAAGGTGTTTATCATAAAAA

FIGURE 116

MPLLKLVHGSPLVFGEKFKLETLVSACIPVFRRLARRRKILFYCHFPDLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRITSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTF LRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACC**ATG**TTGGACTTCGCGATCTT
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGAAGTTTGTCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCGTGGT
 CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC
 ATATCAATCCCAATAAGACATCGGACCCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCATGAGGAAAAAATTGTATGAAAATGGTGT
 GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTTCTAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCCG
 CTTCAGAGAATCATGGCACAGTTTGGTCTGAGATTGGAAGGCTTTCTAGATGGGTCAC
 TTGATAAAAAACATGACTCGGAAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTAACCACTCTGAA
 GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGAAATGGTCTGTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAACTGTTGAACTGCCA
 AACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATT
 CCTAGAGAGACCCTCGTCTTTATGCCCTTGGTGTGTAATTCAGGATCCTAATACTTGGCC
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATAGTAATGAAACTTTTTCTCT
 CACTTGGATTCTCAGGCACACAGGAGTGTCAGAGTTGAGGTTTGCATATATGGTGACCACA
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTATTGA
 AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
 ATT**TAA**ATTTTATACATTTAAATCATTTGTTAAATTGATTGAGGAAAACAACCATTTAAAAA
 AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC
 TTAA

FIGURE 118

MLDFAIFAVTFLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLVVS LGTVDLKQHINPNKTS DPFETMLKSLRLYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLLLKSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQEVIRFQKNHGTWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLT TSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL
QDPNTWPSPHKFDPDRFDD ELMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGA
GACCGCCGCCCTTGTCCTCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTCCTCTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT
ACAGGCCTGCCTGCCTCTCACGTTCAACCCCGAGGAGTATGACAAGCAGGACATTCAGCTGG
TGGCCGCGCTCTCTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCATACGTATTGGTACATTTTTGTCT
TCTGCAGTGCCCTTCCAGCTGTCACCTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAA
AAGAAACCCTTCTGATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
CCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA
ATTAAAAAAAAAAAA

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCASVALSFFIFERWECTTYWYIFVFCSALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 121

TCCCGGACCCCTGCCGCCCTGCCACT**ATG**TCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
GTGCCCCGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCGCCTCGTGCCAGC
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCACGTGGGCTAC
AACTTCCTGATTGGAGAAGACGGGCTCGTATACAGGGCCGTGGCTGGAACCTTCACGGGTGC
CCACTCAGGTCACCTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG
ATCGGGTGCCACACCCAGGCCATCCGGGCAGCCAGGGTCTACTGGCCTGCGGTGTGGCT
CAGGGAGCCCTGAGGTCCAATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TGA**GGCC
CTGCTGATCCGCACCCCATTCCTCCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA
ATAAGATGTAGCTC

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDFACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLAGGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACT
 GACTCGTGCTGCTTCGTGTTCCCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCTCCCGGCTCAGAGGACCTTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC
 CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCATGGCCAATTCCACTCT
 CCTAGGGCTGCTGGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
 CGAACCACAGCCCCCACCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCACCAGGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGAGCCT
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCAGGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCAGGACTAT
 CGGCTGTGCCAAGAGGTGTGCCAGATTACAACCTACCATAGTGATACCCCTACTACCCATC
 TGGGTGACCCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCCTGCCATGC
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTTGGGCCTCAGGCAGGAGAGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGTCCTCAAGTG
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGAGTGGGCT
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCTGTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCC
 ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGTGGCTCCTCTGGGAG
 CATCCATGTGCCGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTGACACCGGGGTTCTCC
 CGGATGTGATGGCGCCGCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCGGGCCGAGCA
 GCATGTGCTGGATCTGTTCTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGT
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTCTTGAGCAGGAAATAAGCTT
 GCCCCGGGGCA

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLLYLICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGR
RTSLCTHDPKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPY
YPSG

Important features of the protein:**Signal peptide:**

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCCA
 GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
 TGGTGAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG
 CATCTTCCCAGCACC GGATCCCGGGTAGGAGGCGACGCGGGCGAGCACACGCGCCAGCC
 GGCTGCGGCTGCCACACGGCTCACC**ATG**GGCTCCGGGCGCGGGCGCTGTCCGCGGTGCCG
 GCCGTGCTGCTGGTCTCACGCTGCCGGGGCTGCCCCGTCTGGGCACAGAACGACACGGAGCC
 CATCGTGTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG
 GCTCCTCTTCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTGCGCTTCTCG
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT
 CGATCAGATCCTGGTGAATGTGGGTAATTTTTTCACATTGGAGTCTGTCTTTGTAGCACC
 GAAAAGGAATTTACAGTTTCAGTTTTCACGTGATTAAGTCTACCAGGCCAACTATCCAG
 GTTAACCTTGATGTTAAATGAAAAACAGTAATATCTGCCTTTGCGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGTTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
 AACTGGAGAAAGTAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTCTGGCTTTCTGGTG
 TCCCCCTA**TAG**GATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGAAGATCATTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG
 TGTGCTGTTTACGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
 ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTCAATTCCTGGGATTACTGAATTAGT
 TACAGATGTGGAATTTTATTTGTTTAGTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAACCTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG
 TGTAAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGTGTTCTTGTA
 AAACTTGGATTTTTTTTTTTCAGTAACGGTATTATGTTTTCTCTTAAAAAAGGTAATGAA
 TGGCTTGCCACAAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAA
 GAATGCTTCATAGTTGTATTTAATTGTATATGTGAAGAGTCATATTTTCCAAGTTATATT
 TTCTAAGAAGAAGAAATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCCTCCGAGGGAAATCTTATACTTTATTGC
 TCAACTTAATTAATAATGATTGATAATAACCACTTTATTA AAAACCTAAGGTTTTTTTTTT
 TCCGTAGACATGACCACTTTATTAACGGTGGTGGGATGCTGTGTTTCTAATTATACCTAT
 TTTTCAAGGCTTCTGTGTATTGTAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA
 TATATTTATCTGTTTAGCTAATATTAATTCAAATATCCCATATCTAAATTTAGTGCAATAT
 CTTGTCTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGAATAAAGA
 TTAATATATGTTAAAAAA

FIGURE 126

MGSGRRALSAPVAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSSSPLGI
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIFYFDQILVNVGNFFTLESVVFVAPRKGIIYSFSF
HVIKVYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

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FIGURE 127

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC
 GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC
 TTTCTTCTGGTTGGTGTCTCTACTGATTTCGTCCCTTGTTGGTTCATGGCAAGAGTCATTA
 TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
 TATATCCAAGAAATGTTCCGATTTCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
 GAAGAGTATAAAACCAGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
 TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG
 CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCTTTATTCAGCTTTCATGAC
 GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGATGGCTGTGAGAAGA
 AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
 ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGTCTATGGGCAC
 CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
 ACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGATTAACCCTCAGGAACCAGCACTTCCCAA
 ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTCTG
 GTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 128

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLG
GIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKCLLCQDKN
FLLYNQRSR

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACCAGCCGCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTTCGCTCTGGGGCTTGCCCTTCTT
 TGGTGCTCTTGGTGGCCTCGGTCSAGAGCCATCTGGGGGTTCTGGGGCCCAAGAACCTCTCGCAGAAAGACGGCC
 AGTTTGTAGCGCACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACATATCTGTGTGACCC
 GCAACAGCAGCAGAGGGGCGTGGTGTCTGTGAACGTCTGAACAGCAGAGAGGGGGCGCGCTTGTCTTTGTGGG
 TCCGCCAGAGAGGAGCTGTGGTGTCTTCCAGGTGCCCTAATCTCTGCGAGGGATGTTTTCAGCGCAAGTACCTCT
 ACCAAAAAGTGGAAAGCAACCTCTGTGACGCCCCCACCAGAATGAGTCGGAGATTTCAGTTCTCTACGTGGGATG
 TGTCCACCTGTGACCACTCAACACCACATACCAGCTCCGGGTGAGCCGATGGACGATTTGTGCTCAGGACTG
 GGGAGCAGTTTCAGCTTCAATACCAAGCAGCAGAGCCGACTCTCAAGTATGAGTTCCTGAAGCGCTGGACT
 CGGTAAATTTCAAGGTGACCTCCAAACAAGGCTTCCCTGCTCAGTCACTCCATTCAAGGATGTGCTGTGCTG
 TCTATGACCTGGACAACAAGTAGCCTTCATCGGCATGTACAGACGATGACCAAGAGGCGGCCATCACCGTAC
 AGCGCAAGACTTCCCGCAGCAACAGCTTTATGTGGTGGTGGTGAAGACCGAAGCAAGCGCTGCGGGGGCT
 CCTGCTCTTACCCCTTCGAGAGATGAACCGGTGATCAAGGGCAGCGCCAGAAAACCTCTCAGTGTCTGG
 TGTCTCAAGCAGTCACGCTGAGGCATACGTGAGTGGATGCTCTTTGCTGGGTATATTTCTCTCTTTTACC
 TGCTGACCGTCTCTGGCTGCTGGGAGAACTGGAGCAGAGAAGAAGACCTGCTGGTGGCCATTGACCGAG
 CCTGCCAGAAAAGCGGTCAACCTCGAGTCTGGCTGATTCTTTCTGCGAGTTCCCTTATGAGGGTTACAAT
 ATGGCTCCTTTGAGAATGTTCTGGATCTACCGATGCTGCTGGTTCAGACGCGTGGCAGTGGGAGCTCTCTTACG
 GTTACAGGGCGCTCTTTGAACCTGTAGGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATG
 ACTACGACACATTGACCGCATCGATTCCGACAGAATGTCATTTCGACCAAGCAATACCTCTATGTGGCTGACC
 TCCACGGAAGGACAGCGTGTGTCGGGAAAAGTACCAGTACTCTTCTGGAACATTGCCAACCTGCTGTCT
 TGTATGCCCTCTCTGTGGTGACGCTGGTGATCACTACCAAGCGGTGGTGAATGTCCAGAGCAATCAGGACATCT
 GCTACTACAATTTCTCTGCGCCACCACCTGGGCAATCTCAGCGCTTCAACAACATCTCAGCAAGCTGGGGT
 ACATCTGTCTGGGCTGCTTTTCTGCTCATCATCTCTCAACGGAGATCAACAACAACCGGGCCCTGCTCGGCA
 ATGACCTCTGTGGCTGTGATGTGGGATCCCAACAACATTTGGGCTTTCTACGCCATGGGCAAGCCCTGATGT
 TGGAGGGGCTGCTCAGTGCTTGCTATCATGTGTGCCCAACTATACCAATTTTCAGTTTGCACACATGTTCAATG
 ACATGATCGCGGACTCTGATGATTCGAGCTCTACCAAGCGCAGCCGACATACCGCCAGCGCTCAGAGT
 CCTACGCTGCTCGGCCATCTGCTCATCTTCTCTCTGTGCTGGGCTGGTCTTTGGCAAGCAGCAGCGGCTCTCT
 GGATGCTCTTCTCATATTGACATCATCGCCACCTGCTCTCAGCAGCGAGCTCTATTACATGAGGCGGGTGA
 AACTGGAATCGGGAATCTCCGCGCATCTTCCACGTGCTCTACAGACTGCTCAGTCCGCGAGCTCGAGGCGGCG
 TCTACGTGACCGCATGTTGCTGCTGCTGATGGGCAAGCTCATCACTGCTGGTGGCTGCCATGAGGCTTATCA
 TCGCCCCAATGATTTGCTTCTCTACTTGTGGCCATTGGCATCTGCAACCTGCTCTTACTTCCGCTCTTACA
 TCAICATGAGCTCCGGAAGTGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATGCTTTGCACCTCCGTGGTCT
 GGGGCTTCGCGCTCTTCTTCTTCTCCAGGGACTCAGCACTGGCAGAAAAACCTCTCAGAGTGGAGGAGCACA
 ACCGGGACTGCATCTCTCGACTCTTTGACGACCAGCAGATCTGGCCTCTCTCTCTCATCGCCATGCTTCTG
 GGTCTCTCTGGTGTGCTGACACTGGGATGACGACTGGATACITGTGACAGCGGACAAGATCTGCTTCTTAGC
 AGGAGCTGGGCGCTTGGCTTCACTCAAGGGGCGCTGAGCTCTTTGTGTATGACAGCGCTCACTCTGTCTGTGCT
 GTGGGATGAGTCCAGCAGCGCTGCCAGCAGTGGATGGCAGCAGGACAGGCTGATGCTTAGGCTTGGCCCT
 GGGACAGCCATGGGTGGCATGGAACCTTGACGCTGCCCTCTCGCAGGAGCAGGCGCTGCTCCCTGGAACCCCC
 AGATGTGGCCAAATGCTGCTTCTCTCAGTGTGGGGCTTCCATGGGCGCTGCTTGGCTCTCCATTT
 TGCTCTTTGCAAGAGGAGGATGGAAGGACACCTTCCCATTTTCACTGCTTGCATTTTGGCCCTCTCTCTCCCC
 ACAATGCCACGCTCGGACCTAAGGCGCTTTTTTCTCTCCATACCTCCCACTCAGGGGCTAGTCTGGGCGCTGA
 ATCTCTGTCTGTATCAGGCGCCAGTCTCTTTGGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 AGGATGGATGGGGGTATGAGATTTTGGGGGTGGCGAGCTGGTGGCAGTTCAGTTCAGTTCAGTTCAGTTCAG
 CTGGGCGAGTGGCTGATTCTCTCTCTGACCTGTGCTCAGGGCTGGCTCTTTAGCAATGGCGCTCAGGCCAAT
 TGGAGACCGCTTGTATTCAGAGGCTGAATCAGAGGTCACTCTTCACTCAGCTCCAGACTCCAGACTGAGC
 AGCAGCAGGACTGGAGGGAAGAGCGCTTACCCCTTCCCTTCTCTTTCAGGCGCTTAGTCTTGCACAAACCC
 AGCTGTGGGCTTTTCAAGTGCTTACACTGCCCCAAGATGTCCAGGGCAAGAGGAGGATGATACAGAGTTTCAG
 CCGGTTCTGCTCTCAGAGCTGTGGGCACCCAGTGCTACCTTAGAAGGGGCTTTCAGGAGGAGTGTGCTGTTT
 CCTCTACGTGCCAGCTCCAGCTCGCTCTAGGACCCAGGGCTGGCTTCTTCAAGTTCCTGCTGCTTCTCAGGCA
 AGTTCTGTGTAGTCATGCACACATACCTATGAACCTTGGAGTTTACAAAGATTCGCCAGCTCTGGGCAC
 CTGGGCCACCTGGTCTGGATCCCTCTGCTCCACCTGCTCCACCCGATGTAGGATGGGGAGCTCAGG
 CGGGGCTCTGCTTTGGGATGGGAATGTGTTTTCTCCAAACTGTGTTTTATAGCTCTGCTTGAAGGCTGGG
 AGATGAGTGGGTCTGGATCTTTTCTCAGAGCTGAGGCTGATGTTGCTGCTTCCGTTTTCTATGAATGAAT
 TGCATTCAATAACACAGAGCTCAAAAAAAAAAAAAA

FIGURE 130

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTEGEQFSFNTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFFPCSVISIQDVLCPVYDLNNVAFIGMYQTMTKKAAITVQRKDFPSNSFYVWVV
VKTEDQACGGSIPFPYFAEDEPVDQGHRQKTLVLVLSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLLVAIDRACPESGHPRLVADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGTTRPVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVVTGNQDICYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRALLRNDLCALECGIPKHFGFLFYAMGTALM
MEGLLSACYHVCNPYTNFQFDTSEFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNATFAWIVFSIIHIIATLLSTQLYYMGRWKLDSGIFRRILHVLTYTDCIRQCSG
PLYVDRMVLVLMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFFQGLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF
```

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCTTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTGT
 ACCATGGCTCCCTGCGCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGC
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCAGAAAACTATGGTGGAAATTTCCCTTTATACC
 TGACCAAGTTGCCGTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGCAGGGGACTCA
 GGCAGAGCAACTGAGGGCCATTGCTATGGATCCAGATTCTGGCTTCCCTGGTGACCAAG
 GGCCTTGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATG
 GACATGCTTTGTGGGCTCCACAGCCTGTGCTTGTGCAGTGAAGGATGAGAATGACCAGGTG
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGTACCGGCCCTGGCATCCC
 CTTCTCTTCTTGGAGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT
 TCCACATCTCGAGCCAGGCTCCAGCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCCTCAGGCCACCAGGCCACTG
 CCACCGTGGAAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
 GAGAATCTCAAGTCCATATCCCGCACCACATGGCCAGGTACATGGATGGGGGTGATGTG
 GCACTATCACCTGGAGGACCATCCCCGGGACCCTTTGAAGTGAATGCAGAGGGGAACCTCT
 ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGTCTCAGGTGCGGGCTCAG
 AATTCCCATGGCAGGACTATGCGGGCCCTCTGAGAGCTGCACGTGCTGGTGATGGATGAGAA
 TGACAACGCTGCCATATCTGCCCTCCCGTGACCCACAGTCAGCATCCCTCAGCTCAGTCCAC
 CAGGTACTGAAGTGAAGTACTGACAGTGTACAGCAGAGGATGCAGATGCCCCCGGCTCCCCAATTCC
 CAGCTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCCTTCCA
 GGTGGAGCCCACTTCAGGCAAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACCA
 TCCTGCTTCTGGTGCTGGCCATGGACCTTGGCAGGCGCAGAGGGTGGCTTTCAGCAGCAGTGT
 GAAGTCGAAGTGTGCGAGTCAAGATATCAATGATCACGCCCTCAGTTCATCACTTCCAGAT
 TGGGCCATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGGCGCATGTCAACAGGCCA
 TTGATGCTGACCTCGAGCCCGCCTTCCGCCCTCATGGATTTTGCCATTGAGAGGGGAGACACA
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA
 AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCCAAGTTGGACAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC
 AGCCGGCTCTTTCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCCT
 CCGTATCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTTCCGGGGAGGTGCACACC
 GCCCAGTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGGCCAGGA
 TACAGCCCTGACTCTTGCCCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAGACCATG
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCGATCTGGCCAGTGGGACGGGTCCCTCAGC
 TTCACCTTGGTCCCAACCCACGGTGCAACGGGATTTGGCGCTCCAGACTCTCAATGGTTC
 CCATGGCTCACTACCTTTGGCCCTGCATTGGGTGGAGCCAGTGAACACATAATCCCGGTGG
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCTGGTTCGAGTGATCGTGTGCTGCTGCAAC
 GTGGAGGGGACGATGCATGCGCAAGGTGGGCGCATGAAGGGGATGCCACGAAGCTGTGCGGC
 AGTGGGCACTCTTGTAGGCACCTGGTAGCAATAGGAATCTTCTCATCTCTATTTTCAACC
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCTGAAGGCG
 ACTGTCTGAATGGCCAGGCAGCTTAGCTGGGAGCTTGGGCTCTGGCTTCTAGTGTAGTCCC
 CTGGAGAGAGCCAGCCAGCCCAAGATCTCAGCAGGGGACAGGACAGAGTAGAAGCCCTTCCAT
 CTGCCCCTGGGGTGGAGGCCACCATCACCATCACCAGGCATGTCTGCAGAGCGCTGCACCCAAC
 TTTATGGACTGCCATGGGAGTGGTCCAAATGTCAAGGTGTGTGCCCAATAATAAGCCCCA
 GAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 132

MVPAWLWLLCVSVPQALPKAQPaelSVevPENyGGNFPLYLTkLPLPREGAEGQIVLSGDSG
 KATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
 HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSDFMQLEPRL
 GALALSPKGSTSLDHALERTYQLLVQVKMDGDAQSGHQATATVEVSIIESTWVSLEPIHIAE
 NLKVLYPHHMAQVHWSSGGDVHYHLESHPPGPFevNAEGNLYVTRELDREAQAEYLLQVRAQN
 SHGEDYAAPLELHVLVMDENDNVPICPPRPDPTVSIPELSPPGTEVTRLsAEDADAPGSPNSH
 VVYQLLSPepEDGVEGRAfQVDPTSGSVTLGVLPLRAGQNIllLVlAMDLAGAEGGFSSTCE
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMlTAIDADLEPAFRlMDFAIERGDTE
 GTFGLDWEpDSGHVRLRLCKNLSYEAAPSheVVVVVQsVAKLVGPGPGPGATATVTVLVERV
 MPPPKLDQESYEASVPISAPAGSFLlTIQPSDPIsRTLRFSLVNDSEGWLcIEKFSGEVHTA
 QSLQGAQPGDYYTVLVEAQDTAlTLAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
 TLGNPTVQRDWRlQTlNGSHAYlTLALHWVEPREHIIPVVVSHNAQMWQLLVrVIVCRcNV
 EGQCMRKVGRMKGMPTKLsAVGILVGTlVAIGIFlLlIFThWTMSRKKDPDQADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTTCTGGAAATCTCCCTCCCTCTCT
 TCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTGAGTCTGCAGGCATTTAAATCCTTCTCTG
 AGATCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA
 AGATGATGAATGCAACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACCGGG
 CTTACCATTCTCTGGGAAGCTATTACCACGAGATGGACAACATTTGCCGACAGCTTTCTTGAC
 CTGGCGAGGAGGTGAAGATTGGACATTCGTTTGA AAAACCGGCCGATGTATGTACTGAAGTT
 CAGCACTGGGAAAGGCGTGAGGGCGCGGCCGTTTGGCTGAATGCAGGCATCCATTTCCGAG
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTCTTGTGGCTGTGGCCAAATCC
 TGATGGATATGTGTATCTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC
 CTGGAAGCTCCTGCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTTGACGAGAAAG
 GGAGCCAGCGACAACCCCTTGCTCCGAAGTGACCATGGACCCCAAGCAATTCGGAAGTGGA
 GGTGAAATCAGTGGTAGATTTTATCCAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC
 ACAGCTACTCCGAGTGCCTGATGTATCCATATGGGTACTCAGTCAAAAGCGCCAGATGCC
 GAGGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTGGGGCACTGA
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGTAGCGGGAGCAGCATCGACTGGG
 CGTATGACACCGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTTATGGC
 TTCTCTCTGCCAGCTAACAGATCATCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACCTCTACTAGCGCATGGCTCTGCTCTGTCTACATTTAT
 TTGTACCCACAGCTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCATCCTGTGTGAG
 TCAGAGCCCTCTGGGTTTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CGTGTGCTCTGGCGGTGCTCCCTGCAAGAACTGGTTCTGCCAGCTGCTCAATTTTGGTCTCTG
 CTGTTTTTGAAGAGCCTTTTGTCTGTTTCTCCTTCCACCTGCTGGCTGGGCGCTGCACCT
 AGCATCACCCCTTCTGGGTGGCATGTCTCTCTCTACCTCATTTTTAGAACCAGAAACATC
 TGAGATGATTTCTACCCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT
 GTGGGAGACCACTATGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCCCTTTAATTTT
 TCGCAGTCTTCTCGGAAAATATTTTCTTTGAGCAGCAAATCTTGATAGGATATCAGTGAAG
 GTCTCTCCCTCCCTCTCTCTGTTTTTTTTTTTTTTTGGAGACAGATTTTGCTCTTGTGGC
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCAACCTCTGCTCTCTGGGTTTCAAGCA
 ATTCTCTGCTCAGCCTCTTGAGTAGCTTGTTTTATAGGCGCATGCCACCATGGCTGGCTA
 ATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCA
 ACCTCAGGTGATCTGCCCTCCTTGGCCTCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG
 TGCCGGGCCGCTCCCTCCTTTTTTAGGCTGAATACAAAGTAGAAGATCACTTTCTCTCAC
 GTGCTGAGAATTTCTAGATACACAGTTCTTACTCCTCTCTTCCCTTTGTTATTCAAGTGTG
 ACCAGGATGGCGGGAGGGGATCTGTGTCTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA
 GTGACCATCTAAATTGCAGGATGGTGAATATCCCATCTGTCTTAATGGGCTTACCTCCT
 CTTTGCTTTTTGAACCTACTTCAAAGATCTAGGCCTCATCTTACAGGTCCATAATCATCAT
 CTGGCTGGATAAATCTACCTGCCCTGGCACATTTCCATTTGGCTGTGGGTGATCCTGTGTT
 TCCTTGTCTGGTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
 TCTGCTATTTTTGTATCTGGACCACAAGTTCTTAAGTAGAGCAAGAATTATCAACACAGCT
 GCCCTCTGTTTTCTTTCACTCAGCAGTACCATCTGCTCTTTGTTGTTGTTGTTGTTGTTGTT
 TTGTTTTTTTGTCTTTTACCAAACATGTCTGTAATCTTAACCTCCTGCCTAGGATTTGTACA
 GCATCTGGTGTGTCTTATAAGCCAATAAATATTCAATGTAAAAAAAAAAAAAAAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDEMQHNEGQERSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRPAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDIFIQKHGNFKGFIDLHSY
SQLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLPANQIIPTAEETWLGLKTIMEHVRDONLY

Signal peptide:

amino acids 1-16

[illegible]

FIGURE 136

MASYLYGVLFAVGLCAPIIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP
SKDLTLKMGSAFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQSK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMHQKEQFAF
GVDTELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

[illegible]

FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTTSANTGSSVISSGASTATNSGSSVTSSGVSTATI
 SGSSVTNNGVSIVTNSEFHTTSSGIATNNEFSTASSGISIATNSESSTTSSGASTATNSE
 SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
 TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
 SNGAGTATNSESSTTSSGASTATNSDSSSTVSSGASTATNSESSTTSSGASTATNSESSTSS
 GASTATNSDSSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA
 NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSSTSSEAST
 ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
 SEAKPGGSLVPWEIFLITLVSVVAAGLFAGLFFCVRNLSLRNTFNTAVYHPHGLNHGLGP
 GPGGNHGAPHRPRWSPNWFWRPVSIIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
 CCAGCAATATGCATCTTGCACGTCCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
 CTGTCTGGATGGGCGGCCAGCGATGACCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG
 GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGC
 ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC
 AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
 CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
 CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC
 CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
 AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
 TGCAGAAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
 AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCAACCACGCCGTTAGCCTCTGG
 GGCTCAGTCAACACGCCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
 TGCCCTTAAACTGGCATCCGGCCTTGTCTGGGAGAATAATGTGCGCGTTGTACATCAGCTGAC
 ATGACCTGGAGGGGTTGGGGGTGGGGGACAGSTTTCTGAAATCCCTGAAGGGGTTGTACTG
 GGATTTGTGAATAAACTTGATACACCA

FIGURE 140

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHG VNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGV NQASKEANQLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

CTCCGGGTCCGACCGAGGGGCTCCGGGGCCGGCTGTGCAGGGGGGACGAGTCACTGGACACTACAGAGCGAGCC
CCCGCGGGGGGACGATGACCTGCTGCTGACCTGACCTGCTCCAGGTCCGAGCGGGGGCCCCGGGGCGACTCG
GGGGCGGACCCGCGGGGCGAGCTGCGCCCGCTGAGTCCGCGCGAGGCCACTGAGCCGCGAGCGCGGAGACACCGTCT
GCTCTGCTCTCCGACATCGCTCGCGACCGGATGGGGCTGAGGAGCTGCTCTGCGCCGCCCTATGGGGCGCGCTGGCG
CTCTCGGCCACCGCTGCTGCTGCTCTGCTGCTGCTGCTGCTGACGAGCCGCGCTCCGAACTCGSGCGCTCAGC
CCCGCGATCAGCTGCTGCTTGGGCTCTGAAGAGCGGCCTCACTTCAGATTGCAAGGTGACACATCTTCCAATCACT
ACAGCCCTTCTGTGTCAGGAGATGGCAGACCTCTAGCTGGTGTGTCAGAGGCCCTTTTGTCACTCAGTAGC
AACTCAGCTCTCTGTCAGGCGGGGATACCAAGGCTGCTTTGGGTGTCAGACGAGGAAGAAACAGCATGTGCG
AGCTTTCAAGGSCAAGGACCCACAGCGCATGTGCAAACTACATCAAGATCTCTCTCGCGTCAGCGGCGATCA
CTTTTTCACCTCTGGCAGCAGAGCTTCAGCCGCGCTGTATCATCAATCAATAGAGAACTTCACCTCTGCGAAGGG
GACGAGAAGGGGAATGTCTCTTGAAGATGGGAGAGGGCGCTTTGCTCTTGACCCGAATTCAGAGTCCACTGCC
TGTGGTGTGTATGGCAGCTCTACACTGGAACATCAGCACTTCCAAGGAAATGACCCGGGCTACTCGCGGAGC
CAAGCGCTTGCGCCGCCAAGACGAGAGTCCCTCACTGGTGCAGACCCAGCTTTTGTGGCTCAGCTCACT
ATTCTGTAGAGCTGGGCACTTGCAAGGGCGATGATGACAAGATCTACTTTTCTCAGAGCACTGCCAGGAA
TTTTAGTCTTTTGAAGACCAATTTGTGTCGCGATTTGCCGCTATCGCAAGGCGATGAGGGTGGAGAGCGGGTG
CTACACGACGGCTGGACCTCTCTCTCAAGGCCGACCTGTGCTGTACGCGCGACGTGAGTGGCTTCCCTTCAAC
GTGCTGAGAGTCTTCTTCAGCTGAGCCCAACCCAGGACTGGCTGACACTTTTCAATGGGTTTCACT
TCCGACTGGGCAGGGGAACTCAAGAAGCTCTGCGCTGTGTCTTCAAAATGAAGGATGTGACGAGATCTTC
AGCGGCTCTCAAGAGGCTGAACCTGGAGACACAGCATGCTGTACCTGAGCCACCGGTGCCCAACCCGGG
CTGGAGCGTGCTCATCAACAAGTCCCGGAGGAAGGAATCAACTCATCCCTCAGCTCCAGACCGCGCTGTGTC
AACTTCTCAAGGACCAATTCCTAGTGACGGGAGGAGCTCGAAGCGCATGTCTGCTGTGCGCCACCGAGCTCG
TACCCGCGCTGGCTGTACACAGCGCTGCTTGGCTGTGACACACTAGCATGTCTCTTCTGGGCATCTGGTGA
GGCGGCTCTCAAGAGCAAGTGAAGTGGGTCGGCCCGGGTGACACATTTGAGGAGTCGCAATCTTCAATCGGGA
CAGCCCGCTCGAATATGCTCTTGACAACCAAGCGGGGGTGTCTGATCGGGCTACACTCGGCGGTAGTCACT
TGCCCATCGGCAACTCGAGCTCTATACGAGTCTTGGGAGTGGCTCTGCGCGGGAGCCCTGAGTCTGTGG
AGCGGCTCCAGCTCGAAGCAGCTCAGCTCTACCAAGCTCAGTGTGCCACAGGCGCTGGATCCAGGACATCGAG
GGAGCAGCGCCGAAGAGCTTTGACAGCGGTCTTCGGTGTGTCCCGCTTTTGTACCAAGAGGGGAGAAGCA
TGTGAGCAAGTCCAGTTTCAGGCCAACACAGATGAACATTTGGCTCTGCCCGCTCTCTCAACACTGGGCGACCGA
CTCTGCTGTACGCAACGGGGCCCCGTCAATGCTCGGGCTCTGCAAGCTGTACCACTGGGAGACTGTGTGCTGT
GTGGGACCCCAACAGTGGGGGAGTTTCAGTGTGTGTCACTAGAGAGGGGCTTCAGCAAGCTGGTAGGCACTAC
TGCCAGAGGTGTGGAGAGCGGGGTGCGAGCAACACAGTGAAGGTGGGAGTACCGCTGTATTCATCAGCA
TCGGCTGTGATGTCAGCACTGGTGGGAGAGCGAGCTGGGTGCAGACAGTCTCTCACTGAAGGAGTCTTGTGTT
ATGTGACGCTCTTTTGTGCGCTGCTGCTCCAGTTTATTCTGTCTGACGCGACGGAGACAGCATGAAGA
GTCTTCTGAAGCGGGGAATGTGCGAGGCTGCACCCCAAGACCTGCCCTGGTGTGCTGCCCTTGAGACCGCG
CCACTCAACGCGCTAGGGGCCCTAGACCCCGCTGATCCAGCGAGGTACAGTCCCTGTAGACAGCGCCCCG
GGGGCGCGAGTCTTCACTGATGACGAGAAGGCCACTCAGCATCAAGAGAGTCTCTGTGGAGGTATCCCGAGT
TGCCCGCGGCGCGGGTCCGCTTGGCTCGGAAGTCCGTGACTCTGTGTGTGACGAGCTCACTTCAAGAGAGC
TGCCCTGCTGCTCAGGGGTGTGAATGTCTGGAGAGGGTCAACTGGACCTCCCTCCGCTCTGCTCTCTGTGGAAC
ACGACCTGTGTGCGCGGCTCTGGAGGCTTTGGAGCAGTGTGAGCCTGGCTGTGCTCTCAAGTCAAGTAGGAGTCC
TACCCAGCAGACGCAACACAGCGCTGGCCCGAGAGTCTGTGCCAAATATGGGGGGCTGCTAGGTTGGTGAAG
CATGTGCTCTTATGTAACTGAGCCCTTTGTTTAAAGAAACAATTCAAATGTGAACTAGATGAGGAGGAAG
ATAGATGGCATGACGACCAACCGGCTGCTCCAGTTTATGCGCTCCAGGGGTGCTGGGATGCTCAAAATGG
TTGTTGTAGACAGATTTGAAACCTCTCAACAATGGCTCTTCACTTCCAACTTATCCGCTGCCACGGGCTGCT
CTGTCTCACTGTCAGATTCAGCAACAGCTTTGGGTGCTGGTGGCTTGTGCTTCCAGTCAAGCGAGGATGTAGTTG
TTGTCGCTGCTGCTCCACCACTCAGGACACGAGGCTAGGTTGSCATCGCGCTCTCCAGGCTCTGGGCTCG
GGACCGCACTCTCGGACCTTCCAGCTGTATCAGGCTGTGGCCAGAGGACGACGCGGAGCTCAGGAGATA
TTTTGTGACAATGTAGCGCTTTCTCTCAGTAATCAGGGAAGAGACTTCGAGCTCTTCTCTGTTTGTGCTGTA
GAACCGCTGCGCCCTTCCACCATTACCACTCGCTTCATCTTTGAACTCAAACACAGGAATCAACTGCAC
CTGTGCTCTGCCAGTCCCGATTCCCTCTCACTCTCACTCTCTCTCACTTCTCAAGGATATCAACCACTGCC
AGCAAGAGGGGCTGAATTTATGTGTTTATATCATTTTTAATAAGATGCATTTATGTCAATTTTTAATAAA
GCTCGAAGATTAAGTTTAAAAAATAAAAA

FIGURE 142

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSLAAPWGALPPRPPLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELWGADEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCP
FDPNFKSTALVVDGELYTGTVSSFGNDPAISRSQSRLRPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFSETGQEFEEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFFPNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSQLPDRVLNFKDHFMDGQVR
SRMLLLQPQARYQRVAVHRVPLGHHTYDVLFLGTGDGRHLKAVSVGPRVHIIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSILYQP
QLATRPWIQDIEGASAKDLCASSVSVSPSFVPTGEKPCEQVQFQPNVTNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLVLVGTQQLGEFCQWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPVIIISTSRVSAPAGGKASWGADRSYWKFLVMCTLFVLAVALLPVLFLLYRHRNSM
KVFLKQGECA SVHPKTCPPVLPETREPLNGLGPPSTPLDHRGQSLSDSPPGARVFTSEKR
PLSIQDSFVEVSPVCPRPVRVLGSEIRDSVV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGAGGATGTGACAGCTCGGGCGCGCGGCTACGAAGAGGACGGGACAGGCGCGGTGCGAACCGA
 GCCCAGCCCGCCGAGGACGCGGGCAGGCGGGAGCGGAGCTGCTGTCGCGCGCGCGCTGCTGCGCGCTG
 TGGCGCGCCGCGCTCCCGCGCGGACGCGGGAGGAGCTCGCGCACTCGCGCGCGAGCCGCGCTAGCGCGCGC
 CGGGCATGTCCTCTCTAAAGGCGCAGGCGCGCGCGCGGGGGGGTGTGCGGAAACAAAGCCGCGCGCGGG
 CCTCGGGGGCGCTCGGGGGCCGCGATGGCGCGCGCGCGCGCGCGCTGCCGGGCGCTCGCCGGGCGCGCTCG
 CGCGCTAGGGCGGGCTGGCTCGTGGCGGGGCGAGCGGCTGAGGCGCGCGCGAGCTCGCGGGCGCGGGCG
 GGGCGCGCGCGCGCGCGCGGGAGCGCGCGGGCGATGGCGCGCGCGCGCTGAGCTGAGCTGCTGCTGCTG
 TGCTCGGGCTCGTCTGGGCTCGTGGCTCGCGGCTCGCTCTGCCCCGGGCTTCGAGCTGAAGCGCGCGG
 GCGCCAGCGCGCGCGCGCAGCCCGAGGGCTGCGGCTCGGGCAGGCGCGCGCTCCAGGCGCGCGCGCGCG
 GCGATGCGCGCGGGGCGCAGCTCTGGCGCGCGGCTCGGACCCAGATGGCGCGCGCGCGCAGGAACTTTCTCT
 TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGCGCGTGGCGCGCTACAGAACATGGTCCAGACAA
 TTCTCGGAAAGTTCACTTTCTCAAGTGAGGTTCTGACACATCTGACCAATCCAGTAGTGCCACTACGGG
 GTGTGGAGACTCCTACCGCGCCAGAGAAGTCTTATGATGCTCAAGTACATGCACGACCACTACTTTGGACA
 AGTATGAATGTTTATGAGAGCAGATGATGACGTGATCATCAAGAGGAGACCGTCTGGAGAATCTCTGAGGAGTT
 TGAACAGCAGCGAGGCGCTCTTCTTGGCGAGAGGCTGGGCGACCGAAGAAATGGGAAACTGGCCCTGG
 AGCTGTGTGAGAATCTCTGATGGGGGGGCTGGCGTATCATGAGCGGGAGGTGCTTCGGAGAATGGTGGCGCG
 ACATTTGSCAAGTGTCTCCGGAGATGTACACCACCATGAGGAGCTGAGAGGTGGGAAGGTGTCTCCCGAGGTTT
 CAGGGGTCAGTGTGCTGTGCTCTGATGATGAGTGGCGAGCTTTTATGAGAATACGACGACGACAAAGGGGT
 ACATTAGAGATCTCCATAACGATTAATTCACCAAGCTATACATACCCCAAGCAAAACACCCCTACAGCT
 ACAGGCTCCCAAGCTACATGCTGAGCCGAAGATATCCGAGCTCGGCACTCGCACATACAGCTGACACCGGAA
 TTGCTCGTATGAGCAATACAGCAACACAGAAATTCATAAGAGGAGCTTCAGCTGGGAATCCCTCCCTCTTCA
 TGAGTTTTCAGCCCGCGGACGAGGAGATTCGGAATGGGAGTTCTGACTGGAAATACCTGTATTCGCGAG
 TTAGCGCCGAGCCCGCTCGAAGAGAAATGGACTCCGCGCAGAGGAGGCTTGGACACATTTGTCATGACGTCA
 TGGAGATGATCAATGCCAACGCGAAGACGAGGCGAGGCGCATTTGACTTCAAGAGATCCAGTAGCGCTACGCGC
 GGGTGAACCCATGATTTGGGGCTGAGTACATCTGAGCCTGCTGCTTCTGTACAAAGACCAAGGGAGAGAA
 TGACGCTCCCTGTAGGAGGCGCGCGTATTTACAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAG
 TGGATGCACAGAGCTTGGCCAGAGAAATCAATCAGGAATCTGGATCCTTGTCTTCTCTCAAACTCCCTGAAGA
 AGCTGTGCTCCCTTTCACTCTCGGTCGAAGAGTGAACACAAAGAACCAAGATAAAAGATAAACATATCTGA
 TTCTCTTGTCTGGGCTTTGCACATGTTTGTGAGATTTATGGGAAATTTGAGAAGACGTGCTTATCCCCAATC
 AGAAGCTCAAGCTCGTGCTTCTGCTTTTCAATTCTGACTCCACCCCTGACAAGGCCAAACAGTTGAATGATGA
 GAGATTAACGCAATTAAGTACCCCTAAAGCCGACATCGAGATTTGCGCTGTGTCTGGAGATTTTCAAGAGCCCTGG
 CCCTGGAAGTAGGATCTCGCCAGTTTAAACATGAATCTTTGCTCTTCTCTGCGAGCTCGACCTCGTGTTTACTA
 CAGAATTCCTTCAGCGATGTGCGAGCAATACAGTTCTGGGCGAACAATATATTTTCCCAATCATCTTCAGCCAGT
 ATGACCCAAAGATTGTTATAGTGGGAAAGTTCCCAAGTGAACCATTTTGCTCTTACTCAGAAAACTGGCTTTCT
 GGAAGAACTATGGGTTGGCATCAGCTGATTTATAAGGGAGATCTGTCCGAGTGGGTGGCTTTGATGTTTCCA
 TCCAAGGCTGGGGGCTGGAGATGTGGACCTTTCAACAAGGTTGTCCAGGAGGTTTGAAGCAGCTTAGGAGCC
 AGGAAGTAGGAGTAGTCCAGTCCACCATCTGTCTTTGTGATCCCAATCTTGACCCCAACAGTACAAAATGT
 GCTTGGGCTCCAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCGA
 GTTACAGTAAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCTAATGTCCAGCTTTGCTGGAAAAAGCGTTT
 TAATTTCTATTTTATTTTCCAAAAATTTTTGTATGATCAGTTTTTGAAGTCGATACAAAGGATATATTTTAC
 AAGTGGTTTTCTTACATAGGACTCCTTTAAGATGAGCTTTCTGAACAAGAGGATGATCAGTGTGTGCTTTGAA
 CAGATCTCTTCTGCTGAACATTTATGAGCAGCTGCTTAACCTTTGACTTGAATGACTGATGAACAAACATTT
 TTTAAAAAATGTTTTCTTTGAGACCTTTGCTCCAGTCTTATGGCAGAAAGCTGGAACATCTCTGCAAGATAT
 TATTTGACAAAAACGTAACCTCTGGTAAATGTTCTGTGTGATGTTAACTTCCAGATTCACAGATTCACCTTTGT
 GTTTTGTTTTTTTTTTACAAATGTTTAAAGCCATTTTATGTTCCAGTTGTAAAGTAAAGAAATGATGAATA
 GCTGTTTTCATCATCTCTCAGGAGAGCTTCCAGAGTGTGATTTCTCTCATGCTACTGCTGCTGAGCTGGC
 CAGTAGGTTTTTTTTTTTTTTTTTTTTTTTTTTTGTAGACGGAGTCTCACTCTGTATCCAGCGCTGGAAAT
 CAGTGGCGCAATCTTGCTCACTTTAACTCCACTTCCCTGGTTCAAGCAATCCCTCGCTTTGCTGCCCGGAGT
 AGCTGGGATACAGGACACACACCACCGCCAGNATGTTTTTTGATTTTATGTAAGACGGGGTTTCCACAT
 GCAAGCCAGCTGGCCATGTAGTTTTAAAGCAGGGGCGTGAAGAGGCAGTAGGATGTGGCTGTCTCG
 TGGTAGTTTATTTGCGGCTAAATAGACCTGGCATTAAATTCAGAAGGATTTGCGATTTTCTCTCTGACCCCT
 CTCTTTAAAGGCTAAATATTAACTTTTAAAGTGAACAAAGATATTATTAACATAAATCTGATGTACACAGAT
 GAACATACACACATACACCTTAATCAAACGTTGGGAAAAATGTATTGTTTTCTTCTCTTTCATCCTCTCTG
 TGTATTCTGGTGAGATGTTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
 TTTATTTAATATCTGTGTTGAGAGCTCTGCCATTTCTGAGTACCTGTGATAGTATTATTTATGTCATCTCGG
 GAGTGTGTTTAGTCTGTTTTATTTGAGTAAACCGATCTCAAGATTTCTCTTTGGAAAGCTTTTTCCCTCTC

FIGURE 143B

TTAAATTTTATATTCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAAGTTAAATCTCAGATCAAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGAAAATAG
CCTGATGCTCATTGGAAAAATAAACCAAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT
ATTCTGTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAAGTTAAACACGAAAAAA

FIGURE 144

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLVGVMTAQKYLQTRAVAAAYRTWSKTI PGKVQFFSSEG
SDTSVPPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFWMRADDDVYIKGDRLLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCWVSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQEE
ILEWEFLT GKYL SAVDGP PRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNFMYGAEYILDLLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFLSNSLKKLVFPQLPGSKSEHKPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLEVDLDFNKNVQAGLKTFRSQEVGVVH
VHHVPVFCDPNLDPKYKMC LGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
 TTTCGGCCTTGAGGTTCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
 ACGGACGACGCCT**ATGA**AGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
 CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC
 TAACTCTCCAAAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA
 CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAAATACAC
 ACTTTCCCTACAGGAGGCTTACACCCGGAATAGGAAAGAAAAACACACGGAAGTACCCC
 ATTCTGGTCGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG
 AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATAAAGTCACCTGTAC
 CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
 CAGGTGAACTGCGATAGAAAAACCGAAGAGTTTGAAAGCACCAGAGAGTTGGAATAAT
 GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGA
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAACGAAGCC
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTAATAACAAATGTATAAGTCCAGTTATTGCCA
 GTAGGACGAACAAGTAATAAAATTTGATGACATCGAACTGTTATTAAATGCTGTGTAATTC
 TAGATCTAAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG
 CTGCTACAGTATTCAATACATTAATAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
 AAAGTTTAT**TAA**ACAATAATATAAAAAATTTAAACCTACTTGATATTCCATAACAAAGCTGA
 TTTAAGCAAAGTGCATTTTTTCACAGGAGAAATAATCATATTTCGTAATTTCAAAGTTGTAT
 AAAAAATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTATGAACA
 ATTTTCATATGCACTAAAAACCTAATTTAAATAAAAATTTTGTTTCAGGAAAAA

FIGURE 146

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVSPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEPEYIENEEPEPEPEPAKQTEAPRMLPVVTSSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPLSGETAIEKPEEFGKHPESWNDDILKKILDINSQQQALLSDTSNP
AYREDIEASKDHLKRLALAAAAEHKLKTMYSQQLLPVGRTSNKIDDIE TVINMLCNSRSKL
YEYLDIKCVPPPEMREKAATVFNTLKNMCRSRRVTALLKVY

Signal peptide:

amino acids 1-19

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCCTG
 ACCTCCAAATCATCCATCCACCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACA
 GGAATATCCATGGCCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA
 GTGGCAAGTCACTGGACCGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT
 CCTGCTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGGGTCTCTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
 GTATCGAGGGAGAATGAGTTTGTGAAGGACTCCATTGCAGGGGGGGCTGTCTCTTAAGGC
 TAAAAAATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTTCCAGATTATAC
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCTCTCATTTCCAT
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTCCCCCCAGC
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT
 ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
 AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTTACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTGCATGGGGATGATAATTGTTTTCTTCAAATCCAAGGGAAAAATCCA
 GCGGAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGAAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGGGTTTCTGATCTGAAA
 ACTGTAACCCATAGAAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAGAGATTACAAAGGAA
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
 AAAATGTAGGGTGGTATGTGGGAGTGTGTGGGATGACGTAGACAGGGGGAAGAACATGTG
 ACTTTGTCTCCCAACAATGGGTATTGGGTCCTCAGACTGACAACAGAACATTTGTATTTTAC
 ATTCATCCCCATTTTATCAGCCTCCCCCAGCACCCCTCCTACACGAGTAGGGGGTCTTCC
 TGAGCATGTAGGGGTGGGACCATCTCCTTCTTCAATACAAATGACCACTCCCTTATTTTATACC
 CTGCTGACATGTCAGTTTGAAGGCTTGTGAGACCCATATCCAGCATGCGATGTATGACGA
 GGAAGAGGGGACTCCCATATTCATATGTCCAGTGTCTGGGGATGAGACAGAGAAGACCCCTG
 CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCCACAGGTGGC
 CCCAGCTTCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCCACTCTCCTTTAGGGAGC
 TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGCACTCACAGCTTCCAGATGAGGGGGGAT
 TGGCCTGACCCGTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA
 CATTAGGTTTATGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC
 CAGGCTCCTCATTTTCTAGTACGCGACAGTGATTCTTGCCTCACAGGTGAAGATTAAAGAGA
 CAACGAATGTGAATCATGCTTGCAGGTTTGAGGGCAGAGTGTGTTGCTAATGATGTGTTTTTA
 TATTATACATTTTCCACCATAAACTCTGTTTGCTTATCCACATTAATTTACTTTTCTCTA
 TACCAATACCCATGGAATAGTTATGAAACACCTGCTTTGTGAGGCTCAAAGAAATAAGAG
 GAGGTAGGATTTTTCAGTGATTCTATAAGCCACGACATTACCTGATACCAAAACAGGCAAG
 AAAACAGAAGAGAGGAAGGAAAACCTACAGGTCCATATCCCTCATTAACACAGACACAAAAA
 TTCTAAATAAAATTTTAAACAAATTAACATAAATAATTTAAAGATGATATATAACTACT
 CAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTAAATTTAAATATCAACCAAGTGTAATT
 CAGCACATTAATAAGTAAAAAGAAACCATAAAAAAAAAAAAAA

FIGURE 148

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGK FVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPPSPWRLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELDWRKKGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAGAGTTTGTGGGAACCCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTTTCATTATGTGAGATATAATCAAAGAAGACCTACAA
 TTAATATAGCACATTGTCATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGCTT
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA
 TCTCCATTAAGGGAGAAATTTGTCAAGTCTCAGGTATCAAGTTAGTCAACAGAAGCATGG
 AGTGTGGCTCATATGCTGTTGATTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG
 ATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA
 GATCCTCACTCAGTTAAATTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAA
 GAACCCCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAATGCAGTACATAGAGTTTGTCTCCCTGA
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACT
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTACAGATGCTA
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCCGAAACCCAACAAG
 CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTA
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC
 TGTTTGCTTGATGCATGTATTTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
 CCAGATCAACTCTGTCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCAATTTGTTCTCTAGAAGTTTGTGAGAAATTTGAC
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCCT
 AGCTCCTCTCATTTTCAGCAAATATCCATTTTCAAGGTGCAGAACAAAGAGTGAAAGAAAATA
 TAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTCTTAGT
 GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAAGACAGCAGAATACCAATC
 ACTTCATCATTTAGGAAGTATGGGAATAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA
 TCCTTATTTTCATTTCCAACAACCTACTATGATAAATGTGAAGAAGATTCTGTTTTTTGTG
 ACCTATAATAATTATACAACCTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 150

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYSTLSFTTD
KLYAEFGREASNNTFEMSQRLESMVKNAFYKSPFREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQLHLRQAQVTLIDATTCNEFPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWLIVLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI
```

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
 CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTGAGTGGTGGATTCCCG
 CTGCATCAAGGCCTACCCACTGTCTCC**ATGCT**GGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
 CGTGACCTTCTTGGTTCCAGAGCTCAGCCCTTGCCCCCTCAAGACTTTGAAGAAGAGGAGG
 CAGATGAGACTGAGACGGCGTGGCCGCCTTTGCCGGCTGTCCCTGCGACTACGACCACTGC
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGCGCGCTGCCTGTGCC
 AGGACTCTCCAGCCCCGCCAGCCGCCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
 CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCTCCACTACTGG
 CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCGCTGAACGCTACGGTCCG
 CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATGTCGTTTGCGTAGTGGCCGCTA
 ACGAGGCCGGGGCAAGCCGCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC
 CTTGCCCTTCGGGCCTTGCAAGCCGCCTTGCGGTGCCGCCAACCCCGCACTCTGGTCCACGC
 GGCGCTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
 GCCTGCGGATCGCTGGGGCTGCCCCGCCGAGCCGCCGCCGAGCCGAGGGGCGCT**TGA**
 AAGGGGCTGGGGGCATCTCGGGCACAGACAGCCACACTGGGGCGCTCAGCCTGGCCCCCG
 GGAAAGAGGAAAACCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
 GCTCCAGGGCCACGGCGAGTCATGGTTCTCAGGACTGAGCGCTTGTTAGGTCCGGTACTT
 GGCGCTTGTTTCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCAATTTTTTTTTTA
 AGCGGCCAGATAATAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPLGSSPAQPPDPFRMGVRIAAEEGRAVVHWCAPFSPVLHYWLLWDGSEA
AQKGPFPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRVPAAGGEGLEGADIPAFGPCSRL
AVFPNPRTLVAHAVGVGTALALLSCAALVWHFCLDRDRWGCPRRAAAAAAGAL
```

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAGAACGCTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
 CTGCCCCGATGAGCCCCCGCGTGCCTCCCGACTATCCCCAGGCGGGCGTGGGGCACCAGG
 CCCAGCGCCGACGATCGCTCGCGTTTGGCCTTGGGAGTAGGATGTGGTGAAGGATGGGGC
 TTCTCCCTTACGGGGCTCACAAATGGCCAGAGAAGATCCGTGAAGTGTCTGCGCTGCTGTCT
 CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTGGCAGTTTCTGCTTGGGA
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGATC
 ATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTGTTGCTGTTTCTTATCAT
 TGTGGGATGTTAGGATATTGTGAACGGTGAAGAAGAACTGTGTGCTTCTTGCATGGTACT
 TTGGAAGTTTGCTTGTCAATTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG
 GAACCTATGGTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTA
 TGGATTACCTAGATATCCGTGGCTTACTCATGCTTGGAAATTTTTTTCAGAGAGAGTTAAGT
 GCTGTGGAGTAGTATATTTCACTGACTGGTGTGGAATGACAGAGATGGACTGGCCCCAGAT
 TCCTGCTGTGTAGAGAATCCCAGGATGTCCAAACAGGCCCCCAGGAAGATCTCAGTGA
 CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAATTCCTTTTGGAGAGGAACCAACAACGTC
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAATCCTGGCCATGATTCTCACC
 ATTACTCTGCTCTGGGCTCTGTATATGATAGAAGGGAGCCTGGGACAGACCAATGATGTC
 CTTGAAGAATGACAACTCTCAGCACCTGTCTATGTCCTCAGTAGAACTGTTGAAACCAAGCC
 TGTCAAGAACTCTTTGAACACACATCCATGGCAACAGGTTTAAATACACATTTGAGATGGAG
 GAGTTAT~~TA~~AAAGAAATGTACAGAGAAGAAACCAAACTTGTTTTATTGGACTTGTGAATT
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAATAAAATGTTGCCATAAAATAACA
 CCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCTAAGTCAC
 CACCTGGACAATAAATGATGCCCTTAAATGCTGAAGACAGATGTCTACGCCACTGTGTAGC
 CTGTGTTAGCTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTT
 CGCATGCTGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT
 CTACCAACTAGTATATAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAATACTAATA
 ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATATATATCAGAAAACCTTC
 AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAAATTTCTACCACCTAAAA
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTAAA
 TCTGTATAATTCACTCGATTTCACTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA
 ATTTGTCTGTATAGCATCATTATTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT
 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTGAAAATTA
 CCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTATAA
 GAAAATTTGCACATAACTTAGTTGATTTCAGAAAGGACTTGTATGCTGTTTTCTCCCAATG
 AAGACTCTTTTGCACATAAACACATTTTAAAGGCTTATCTTTGCCTTCTCCAAACAGAA
 GCAATAGTCTCCAAGTCAATATAAATCTCAGAGAAATAGTGTCTTTTTCTCCAGAAAAAT
 GCTTGTGAGAATCATTAACATGTGACAATTTAGAGATTCCTTGTTTTATTCTACTGATTA
 ATATACTGTGGCAAAATTACACAGATTATTAATTTTTTTACAAGAGTATAGTATATTTATTT
 GAAATGGGAAAAGTGCATTTTACTGTATTTTGTGATTTTGTGTTTATTTCTCAGAATATGGAA
 AGAAAATTAATGTGTCAATAAATTTTCTAGAGAGTAA

FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNNVLTLTAE TRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSLDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREP GTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC
 TGCACTCGGGCTCCTCCAGCCAGTGTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCACAGAGCCAGC**ATGT**TACAGGATCCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
 CCCCATCATCATAGCCTACTGAGCCTGGCGAGTATCATCATTTGTGGTTGTCCCTCATCAAGG
 TGATTCTGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCCAGGAAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
 CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGGAACCTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA
 TGTGTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTC
 TCTCAGGCTCCCTGGTCTCCCTGCAGTGTCTTGCCCTGTGGGAAGAGCCTGAAGACCCCCGT
 GTGGTGGGTGGGGAGGAGCCCTCTGTGGATTCTTGGCCTTGGCAGGTGAGCATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACT
 GCTTCAGGAAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGC
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATTCATTGAATTCAACCCCATGTACCCCAA
 AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCTCACTACTTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA
 TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGGCTCAGTCCA
 GGTCAATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA
 TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCC
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
 GGGCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGTGAGCTG**TAA**TGCTGCTGCCCTTTGCAAGTGTGGGAGCCGCTTCCTTCTCTG
 CCTGCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCC
 CTCTGCCACAGCCTCAGCATTTCTTGGAGCAGCAAAGGCCCTCAATTCTGTAAAGACCC
 TCGCAGCCCCAGAGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC
 AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
 GGAACCTTCCCACTACTGAATGGAAGCAGGCTGTCTTGTAAAAGCCCAGATCACTGTGGG
 CTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAAGCCTA
 CTAGAGCAAGAAACAGTTGTAATATAAAATGCAGTGCCTACTGTTGGTATGACTACCGTT
 ACCTACTGTTGTCTATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT
 CTGGCAAAAAAAAAA

FIGURE 156

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALSLASIIIVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELRMRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGGEEASVDSWPQVSIQYDKQHVC GGSI LDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLGSPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTCQGDGGPLMYQSDQWHVVGIVSWGYCGGPSTPGVYTKVSAYLNWIYNVWKAEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCTAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAACGCAGCGGCATCCCCAGGCTCCAG
 AGCTCCCTGTTGACAGTCTGTGGCTGAGCATGGCCCTCCAGGCCCTGGGCTGGACCCCTGGAGCCTCTCGGGCC
 TTTTCTCTTCCAACCTGCTTACGTGCTGCTGCCGACGACACCGCGGGGGAGGCGGGCAGGGGCCCATGCCA
 GGGTCAGATACTATGACGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCTCCAGGATTTTGACA
 CTCTGCTCTGAGTGGTGATGGAATACTCTCTACGTGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGG
 ATCCAGGGGTCCCAGGCTAAAGAACATGATACCTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTA
 AGAAGAAGAGCAATGAGACACAGTGTTCACACTCATCGTGTCTGGTTTCTTACAATGTACCCCATCTCTACA
 CCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAATCAAGATTCTACCTGTTGCCCATCTCGG
 AGGACAAGTCTATGGAGGAAAGGCCAAAGCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATG
 GGATGCTCTATTCTGTTACTATGAACAACCTTCTGGGCAGTGAGCCCATCTGATGCGCACACTGGGATCCGAGC
 CTGTCTCTAAGACCGCAACTTCTCTCGCTGGCTGCATCATGACGCTCTTTTGGCAGCCATCCCTTCGACCC
 AGGTCGCTACTTCTTCTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGGGGTGG
 CTAGAGTCTGCAAGATGACGTGGGCGGCGGAAAAGCTGCTCAGAGAAGTGGACACAGTTCCTGAAGCGCCAG
 TGCTCTGCACCCAGCGGGGACAGTGCCTTCAACGTATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCCA
 CAGCTCCCCACATCTACGAGTCTTACCTCCAGTGGCAGGTTGGCGGGACAGGAGCTCTGCGGTTTGTGCCT
 TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAGAGTTGAACAAGAAACTTCACGCTGGACTA
 CTTATAGGGCCCTTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGGCCCTCTCTGATAAGGCCCTGACCT
 TCTATGAAGACCACTTCTCTGATGGATGAGCAAGTGGTGGGACGCCCTGCTGGTGAATCTGGCGCTGGAGTATA
 CACGGCTTGAGTGGAGACAGCCAGGGCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCAACAG
 GGTCTGCTCCACAAGCTGTGGTAAAGTGGGACAGCAGTGTCTCATCTGGTGAAGAGATTACAGTGTTCCTCGACC
 CTGAACCTGTTCGAACCTGACAGCTGGCCCCACCCAGGGTGCAGTGTGTTGTAGGCTTCTCAGGAGGTGTCTGGA
 GGGTGGCCCGAGCCAACTGTAGTGTATGAGAGCTGTGTGAGCTGTCTTGGCCGGACCCCACTGTGCCT
 GGGACCTGAGTCCCCAACCTGTTGCCTCTGTCTGCCCCCAACCTGAACCTCTGGAAGCAGGACATGGAGCGGG
 GGAACCCAGAGTGGGCATGTGCCAGTGGCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCGCAAACTATTA
 AAGAAGTCTGGCTGTCCCCAATCCATCTCTGGAGCTCCCTGCCCCCACTGTACGCTTGGCCTCTTATTATT
 GGAGTCAATGGCCCGAGCAGCAGTCCCAGAGGCTCTTCCACTGTCTACAAATGGCTCCCTCTGTGTATGATGCGAG
 ATGGAGTTGGGGTCTCTACAGAGCTGGGCAACTGAGAATGGCTTTTCACTACCTGTGATCTCTCTACTGGGTGG
 ACAGCCAGGACCAGACCTTGGCCCTGGATCCTGAACCTGGCAGGCATCCCCGGGAGCATGTGAAGTCCCGTTGA
 CCAGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTCTACTGGCCCACTTTGTCTACTGTCACTGTCTCT
 TTGCCCTTAGTGCTTTCAGGAGCCCTCATCATCTCTGTGGCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAG
 TTCAGGGCTGTGAGACCTTGGCCCTGGGAGAGAAGGCCCGTTAAGCAGAGAGCAACACTCCAGTCTCCCAAGG
 AATGCAGGACCTCTGCCAGTGTGAGCAGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA
 CAGGCCGGGGCTGGGGTGCAGGCACCTGGCCATGTGGCTGGGCGGCCAAGACACAGCCCTGATAGGATGACAG
 CAGCACAAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCACTCACTGATGACACTCAGCAGGGT
 ATGCACAGCAGTCTGGCTCCCTATGGGACTCCCTCTACCAAGCACATGAGCTCTCTAACAGGTTGGGGCTAC
 CCCCAGACCTGCTCCTACACTGATTTGAAGAACCTGGAGAGATCCTTCACTTCTGGCCATTCCAGGACACCTC
 CAGAACACAGTGTTCAGAGACCTTAAAAAACCTGCCTGTCCAGGACCTATGGTAATGAACACCAACATC
 TAAACATATATGCTAACATGCCACTCTTGAAACTCCACTCTGAAGCTGCGCTTTGGACACCAACACTCCCT
 TCTCCAGGGTCAATGAGGATGTGCTCCCTCTGCTTCCCTTACAGTCTGTGACCCGCTGACTCCAGGAAGTC
 TTTCTGAAGTCTGACCACTTCTTCTTCTGCTTCAAGTGGGCGAGACTCTGATCCCTCTGATCCCTGCGCCAGAAAG
 CAGGGGTAACTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACTCTCCCCCTCCCTTTTCTTTGT
 TTTGGGATTAGAAAACCTGCTGTACAGAGACTGTTATTTTTTATTAATAATATAAGGCTTAAAAAA

FIGURE 158

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ
DFTDLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFS PACTFIELQDSYLLPI SEDKVMGKGQS PFDP AHKHTA
VLVDGMLYSGMTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVA AIPSTQVVYFFFE
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGS LHKAVVSGDSSAHLVEEIQLFDPDEPVRNLQLAPTQGA VFVGFSGGVWRVPRAN
CSVYESCVDCLARDPHCAWD PESRTCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQSYWP
HFVTVTVLFALVLSGALIIIVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVDADNNCLGTEVA
```

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAG
 TGAGC**AT**GGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCCTGCTC
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCAACATGCTTAACCACAAAAGAG
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTCTTTCTGGAAGAAACTTTAGG
 TGGCAGAGGAAAAATTTGAAAATTTATTAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
 ATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGGAACCTTCGACATGGTGATA
 GTTGAAACTTTTGACTACTGTCTTCTGATTGCTGAGAAGCTTGGGAAGCCATTGTGTCG
 CATTCTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACCAATCCCTTGTCTTATGTTCT
 CAGTATTCGGTTCTTGTGACTGATCAGATGGACTTCTGGGGCCGAGTGAAGAAATTTCTG
 ATGTTCTTTAGTTTCTGCAAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA
 GGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT
 GGTTCATTAACCTGACTTTTGCTTTGATTTTGTCTGACCTCTGCTTCCCAACACTGTTTAT
 GTTGAGGCTTGATGGAAAACTTATAAACCAGTACCACAAGACTTGGAGAACTTCATTGCG
 CAAGTTTGGGACTCTGGTTTTGCTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGA
 ATCCGGAATCTTCAAGGAGATGAACAATGCCTTGTCTACCTACCCCAAGGGGTGATATGG
 AAGTGTCAAGTTCTCATTTGGCCCAAGATGTCCACCTGGGTGCAAAATGTGAAAATTTGTGGA
 CTGGCTTCTCAGAGTGACCTCTGGCTCACCCAAGCATCCGCTGTTTGTCTACCCACGGGG
 GGCAGAAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAGTTTGGTGTTCATTACAGTT
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCCGCGGAGTGGCTGCCAGTGTCTATCTGCGCTCCCAACCGCTCAGGCCCCACACAG
 CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCAGCGCACTCAAGCCCTA
 TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTGACGCTTTTTGTGTTTCTGCTGGGGC
 TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGGATGGCTGTCTGGTGGCTGCGT
 GGGGCCAGAAAGGTGAAGGAGACATA**AG**GCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG
 GCGATGTCACCAATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC
 TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC
 TAATTTTGTACAAATTCATCCTTACTAGCTCCTGCGCTAGCAGAAATCTTTCCAGTCCT
 CTTGTCCTCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTAGTGACTTG
 GACCAGTACCCCTCAGATTTCAGCCCTTAAATCCACCTTCCCTCTCATCGCCTCTCCGAA
 TCACACCCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCAATATCTTTTCAGTTTCTGTTT
 TGTCTTCCACATATTTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTTCAAGGC
 CGGACACAGGCTCACAGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGTCTCT
 TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAAAATAAAGTTTACA
 GCGTTATCTCTCCCAACCTCACTAA

FIGURE 160

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKGKRP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGGKPFVAILSTSFSGLEFGLPIPLSYVPV
FRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTGSRPVLSHLLLKAELWF
INSDFAFDFAFARLLPNTVYVGGLEMEKPIKVPQDLENFIAKFGDSGFLVLTGSMVNTCQNP
EIFKEMNNAFAHLPGQVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPsirLfvthggq
NSIMEAIQHGVPVMGIPFGDQFENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFLLGLT
LGTLLWLCGKLLGMAVWWLRGARKVKET

```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACATTTCTGTACACCCGTCACACACACATACCATGTT
 CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCCTGAAGCTCT
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTACGCCAGCCTAGAGAGGGC
 AGACTATCAGGGTGCCGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGA
 AGACCGGGGCACTTGTGGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCAAGCCACTGCG
 TACCAGGTCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC
 GGGTGGGCCCAGGAGGGGTCAGAGCCCGTCTGCTGGAGGGGGAGTGCCCTGGTGGTCTGTGA
 GCCTGGCCGAGCTGCTGCAGGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC
 GAGTGGCATTGTGCGGTCCGAAGCCACCACATGAGCCAGCAGGGGAAACCGGCAATGGC
 ACCAGTGGGGCCATCTACTTCGACAGGTCCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC
 CTCTGGCTCCTTCGTAGCCCTGTCCGGGGTGCTACAGCTCCCGTTCCATGTGGTGAAGG
 TGTACAACCGCCAAACTGTCCAGGTGAGCTGATGCTGAACACGTGGCCTGTCTCTCAGCC
 TTTGCCAATGATCCTGACGTGACCGGGAGGCAGCCACAGCTCTGTGCTACTGCCCTTGA
 CCCTGGGGACCGAGTGCTCTGCGCCTGCGTCCGGGGAACTACTGGGTGGTTGGAATACT
 CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTCTGAAGGCCCAAGTCTTTCAAGCACAGAAT
 CCAGCCCTGACAACTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAG
 ACTCCCTCTGGCTCCTATCCACCTCTTTGCATGGGACCTGTGCCAAACACCCAAGTTTAA
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAAGGCCTTTCACCCACCCACCCAGTTACC
 CTCCCAGCCACTGCTGCATCTGTTCTGCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA
 AGAAGGAAGATCTGCACTACTTTGCGGCCCTGCTCCTCCGGTTCCCCACCCACAGCTTCCT
 GCTCAATGCTGATCAGGCACAGGTGGCGCAGGTGAGCCTGACAGCCCCACAGGAGGCCAG
 ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCTGTGAGGAAGCCAGCATCACGGATC
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGTTGGGAGGCTCAGCCAC
 AGGCAGAAGGGTGGGAAGGGCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGTTATTG
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGAGGTAGCAATCCT
 GGCTGTCTTCTATGCTGGATCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTTGTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
 ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAAACTGCTCCAC
 CTTTGAAGTTTGAACCTTGTCCCTCCACACTGACTGCTGCCTCCTTCTCCTCCAGCTCTC
 TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTTTCTCTCTGAT
 CTGTGCTGTCTTATCTCTCTCTTAGGCTTCCTATTACCTGGGATTCCATGATTTCATTCCT
 CAGACCTCTCCTGCCAGTATGCTAAACCTCCCTCTCTCTTCTATCCCCGTGTCCCAT
 GGCCAGCCTGGATGAATCTATCAATAAAACAATAGAGAATGGTGTGCTGAGTACACTAT
 AGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTACAGGTACAGTAGGTA
 TGTTGCAGAGGAAAATAAATATCAAACCTGTATACTAAAAATAAAAA

FIGURE 162

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEPVVLEGECLVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL
```

Signal peptide:

amino acids 1-32

FIGURE 163

FIGURE 164

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSRGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI AVL YFTWL VFDWNTPKKGGRRS
QWVRNNAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHHPHGIMGLGAF CNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTILNRNKG FVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPIITTVGEPITIPKLEHPTQQDIDL YHTMYEALVKLFDK
HKTKFGLPETEVLEVN
```

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 165

GGGCGGCGGGATGGGGGCGGGGGCGGGCGCGGCACTCGCTGAGGCCCGACGACGAGGCCGGGCCGGGCCA
 GGGCCGAGGAGCGCGCGCGGCAGAGCGGGGCCGCGGAGGCGACGCCGGGAGCGCCCGCGGACGAGCAGGTGGCG
 GCGGCTGCAAGGCTTGTCCAGCCGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCCTTGA
 CGGCTGTCTCAGCGAGGGGCGCTGCACCCGCTCCTGAGCAGCGCCATGGGCGCTGTGGCCTCCTGAAGACCCA
 GTTCGTGCTGCACCTGCTGGTCGGCTTTGTCTTCGTGGTGAGTGGTCTGGTCATCAACTTCGTCCAGCTGTGCAC
 GCTGGCGCTCTGGCCGCTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCGCTCGCCTACTCACTCTGGAGCCA
 ACTGGTCATGCTGCTGGAGTGGTGGTCTGCACGGAGTGTACACTGTTACACGGACACCGCCACGGTAGAGCGCTT
 TGGGAAGGAGCAGCAGTCATCATCTCAACACAACTTCGAGATCGACTTCCTCTGTGGGTGGACCATGTGTGA
 GCGCTTCGGAGTGCTGGGAGCTCCAAGGTCTCGCTAAGAAGGAGCTGCTCTACGTGCCCTCATCGCTGGAC
 GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGCCGGACACCGTGGTCAAGGGCTGAG
 GCGCTGTGCGACTACCCGAGTACATGTGGTTCTCTCTGTACTGCGAGGGGACGCGCTTCAAGGAGACCAAGCA
 CCGCGTTAGCATGAGGTTGGCGGCTGCTAAGGGGCTTCTGTCTCAAGTACCACCTGCTGCCGCGGACCAAGG
 CTTACCAACCGCATCAAGTGCCCTCCGGGGACAGTCGAGCTGTCTATGATGAACCTGAACCTTCAGAGGAA
 CAAGAACCCTCCCTGCTGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTTCCTCT
 GGAAGACATCCGCTGGATGAAAGGAAGCAGCTCAGTGGCTTCATAAAGTGTACAGGAGAAGGACGCGCTCCA
 GGAGATATATATCAGAAAGGCATGTTCCAGGGGAGCAGTTTAAAGCTGCCGAGGCGCTGGACCTCCTGAA
 CTTCCGTCTCTGGGCCACCATTTCTCTGTCTCCCTCTTCAGTTTGTCTTGGCGCTCTTGGCAGCGGATCACC
 TCTCCTGATCCTGACTTCTGGGGTTGTGGGAGCAGCTTCTTGTAGTTCGAGAGTCGAGAGATCGCT
 TGAACCTGGGAGGTGGAGATTGCAGTGAAGCTGAGATGGCATCACTGTACTCCAGCTAGGCAACAGAGCAAGACT
 CAGTCTCAAAAAAAAAAAAAACCAAGAAATTCGAGGATTGAACCTGTGTAGTTACTGACATGAAAA
 ATTCACATAGAGGCTGAACAGCAGATTGTGAGCAGGCAGAAAAAATCAGCAAGCTGAAGATGGTACCTTGAGATT
 TTTCAAGGCTAATGAAAAAGAAATGAAGAAAAATTAACAGCCTCAGAGACCCATGTCGACCGTCACACAAATCAA
 CATATGCATGATGAGATCCAGAAAGGAGAGGAGAGAAAGGTCAGAAAGAATGGCCACAAGCTGATGAAAAACA
 GTAACCTACCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTTCAT
 AATCAAAGTGTCAAATGACAAAGAACTTTGAAGCAGCAAGAGATGAGCACTTATCTTGTTCAAAGGATCTTTG
 ATCAGATTAAACAGCTCATTCTCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTGTGAAGCAA
 AACCTCAACTCTAATTAATTTGACTTTTGTAGCTCTAGATGGCTCTGACCTCTTGTCTTCAGGAGCAGATTTC
 ATTTAATCCCTAATAACAATTAAGTCAAGCTTCTTGTAGCTGTAGGAAGGCTGTCTTTAGGCCGGGCACAGTGGC
 TTACACCTCTAATCCAGCACTTTGGGAGGCCAGACGGGTGATCATTTGGGTCAGGCTGATCTCAAACCTCCT
 GAGTTCAGGTGATCTGCCCGCTCAGCCTCCCAAAGTGTGTGATTGCAGGCGTGAGCCACTGCGCTGGCCGGA
 ATTTCTTTTAAAGCTGAATGATGGGGCCAGGCACGATGGCTCAGCCTGTGATCCCAAGTAGCTTGGAATGTA
 AACATGACACCAATGCTGGCTAATTTTGTATTTTGTAGTAGAGACGTGTAGCCAGGCTGGTCTCGATCTCCT
 GACCTCAGTGACCACCTGCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCTGTGCTGGCCTTGA
 GCATCTTGTGATGTCTTATTGGCATTGTATATCTTCTATCTTCTTGGGGAATGTCTGTTCAAGTCCCTTG
 CTTTTTAAATTTTATTATTTATTTATTTATTTATTTTGAAGACAGGCTCTGTCTGTGTCGCCAGCTGGAGTA
 CAGTGGCAGAGCTGTGGCTCAGTCAGCCTCAGCCTCCTGGGCTGAGTGTGATCCCAAGTAGCTTGGAATGTG
 AGCTGTATTTTGTGATTTTGTATTTTGTAGCTGTAGTTTTTGTATTTTGTGGAGACAGCATTTACCATGA
 TGCCAGGCTGTGCTTGAACCTCCTGAGCTCAAGTGATCTGCCTGCTTCAGCCTCCCAAAGTGTGGGATTACAGA
 CATGAGCCATGCACCTGGCAAACTCCCAAAATTAACACACACACAAAAACCACCTGATTCAAATGGGCA
 GAGGGCCGGGTGGCCCACTGAGCTACAGGGGAGACTGAAGTGGGAGGATCGCTTGGGATGAGAAGTCAGAGCTG
 CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACACAGAGTGAGACCTGTCTC

FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVVSGLVINFEVQLCTLALWFPVSKQLYRRLNCR LAYSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCRRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTNLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLN
FLSWATILLSPLFSFVLGVFASGSPLLLITFLGFGAASFVRRLLIGESLEPGRWRLQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTTATTTTTAAGAATCTGAAGTACT**ATG**CATCACTCCCTCCAATGTCTGGGGCA
 GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT
 GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTTGTGGGTTGGTGGCAGGCAGGCCG
 GCTTACGCCTGATACGGCCCTGGGTTAGAAGGAAGGGAAGATAAACTTTTATACAATGGG
 GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT
 TTCTCTAACCTGGCATACCCTGCTTAAAGCCTCTCAGGGCTTCTCTGTCTTAGGATCAA
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTTCATTGT
 ACATGTGGTGTCTCTTGTGCTTCCTG**TAA**TGTGGTATGCCATGGGGTCTTTGCACAAGCCT
 TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACCTTCTCTACTTAATATGTAGTC
 ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
 CTGTGTTAATGCTCTCATAAGACCACTTGTTTCCCTTTTGCACTTGGCCACTCAGTTGTA
 TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC
 TGCGTGAGGGTCAAGGGCATTGCTGTGCTGCCAGGTATAGTGCTACATGTGGTGGGTGCT
 CATGTTTTAGAGACTAAATGGAGGAGAGATGAGGAAAAGATTGAAATCTCTCAGTTACCA
 GATGGTGTAAGGGCCAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA
 TGCAGGTCCTGATTCACTAGGCCCAGGTTGGGCATCTCTAACAACTCCACGTGATGCTGA
 TGCTGGTCTATGAACATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC
 TCACACCTATGATCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
 TCAAGACTAGCCTGGCCAACATGGTGGAACCCCATCTGTACTAAAAATACACAAATTAGCTG
 GGCATGGTGGCACATGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGCAAGAGAAATCGCTTG
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACAGGGTGAC
 AGAGTGAGACTCTATGTCAAAAAAAAAAAAAA

FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSLQCPGAATRHIIHLCVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGLRLLIRPWVRR
EGKINFYTNQDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCAC
 AGGAGTTGAACTGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
 ATTAATACTGTTTTTTGTCTCTTGTAAGTACCTTTACCTTCCTAACACAGAGGATCTGT
 CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC
 ACCGTCCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
 ACCAACTGTCTCAGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGTTA
 GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGAT**TGA**CAAGCCCGAAGATTT
 CATAGGCGATGGCTCCCACCTGCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCCTGGGG
 CCAGGACGGGCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCAT
 CTAACCTTTTCATGTCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG
 AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGCATTCTCTGGAACATGAGGGAACGCCGAGGAAAGCAAAGTGGA
 GGGAAGGAACTTGTGCCAATTATGGGTGAGAAAGATGGAGGTGTTGGGTTATCACAAGGC
 ATCGAGTCTCCTGCATTGAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
 CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGATCCACGTACCAGTGCTG
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG
 CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCCTCCTTCCCTC
 TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
 GCTCAGTGTTGGCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG
 AACACGGAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT
 CAATTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAGGAGCTAGAGCTTGGT
 TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTGTAATTTGAAACCCCAA
 TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG
 CCAACATTTTGGGAGGCCGAGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTG
 GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCCCTGATCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
 GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAAATAAAAAAGAAATTATGGTTATTGTAA

FIGURE 170

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
```

Signal peptide:

amino acids 1-15

FIGURE 171

GCGGGCCCGGAGTCCGAGACCTGTCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
 CCGCCGCTCCTGCCCAGGCCATGACCCCAGCCGGTGCCCCGGCTCTCCGTGCCCGCCGCGCT
 GGCCCTGGGCTCAGCCGCACTGGGCGCCGCTTCGCCACTGGCCTCTTCTGGGGAGGCGGT
 GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCTGTGG
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGTCTGAC
 CCTGGAGCAGCCGAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC
 TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC
 CTGGCCCTGGCCCTGGCGCTGCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
 GCCCCCGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAGATCGACCTCC
 GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC
 GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCCTACTACGAGCGCTGCCTGCA
 GCTGCTGCGACCCGGAGGCATCTCGCCGTCTCAGAGTCCTGTGGCGCGGAAGGTGCTGC
 AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG
 GACGTGAGGGTCTACATCAGCCTCCTGCCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT
CTAGGGCTGGCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC
 CCTGAGTTTTAAATTGAAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

FIGURE 172

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQVPVRLSVPAALALGSAALGAATGLFLGRRCPWPWRGRREQCLLPEDSRLWQYLLSRS
MREHPALRSRLRLTLEQPQGDMMTCEQAQLLANLARLIQAKKALDLGTFTGYSAALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDRLKPALETLDELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

FIGURE 173

CCGCCGCCGACGCCGTACCGCCGCTGCAGCCGCTTTCCGCGGCCCTGGGCCTCTCGCCGTCA
 GC**ATG**CCACACGCCTTCAAGCCCCGGGGACTTGGTGTTCGCTAAGATGAAGGGGTACCCCTCAC
 TGGCCTGCCAGGATCGACGACATCGCGGATGGCGCCCTGAAGCCCCACCCAACAAGTACCC
 CATCTTTTCTTTGGCACACAGAAACAGCCTTCCTGGGACCCAGGACCTGTTCCCTACG
 ACAAATGTAAAGACAAGTACGGGAAGCCCAACAAGAGGAAAGGCTTCAATGAAGGGCTGTGG
 GAGATCCAGAACAAACCCACGCCAGCTACAGCGCCCTCCGCCAGTGAGCTCCTCCGACAG
 CGAGGCCCCCGAGGCTCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGG
 GGGTCACTGGCGTFCACAGCGTAAACGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA
 GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCTGCGCTAAAGATGTC
 GGTCTCGAAACGAGCCCCGAAAGGCCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG
 AAGAGGAGAAGCTCGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACAGGACTTTCACACCT
 GAGAAGAAAGCAGCGGTCCGGGCGCCACGGAGGGGCCCTCTGGGGGACGGAAGAAAAAGAA
 GGCGCCCTCAGCCTCCGACTCCGACTCCAAGGCCGATTCGGACGGGGCCAAGCCTGAGCCGG
 TGGCCATGGCGCGGTTCGGCTCCTCCTCCTCCTTCTCCTCCTCCTCCGACTCCGATGTG
 TCTGTGAAGAAGCCTCCGAGGGGACGGAAGCCAGCGGAGAAGCCTCTCCCGAAGCCGCGAGG
 GCGGAACCGGAAGCCTGAACGGCCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGG
 TGGACCGCATCAGTGAGTGGAAGCGGGGACGAGGCGGGAGGCGGAGCTGGAGGCCCGG
 CGGCGGCGAGAGCAGGAGGAGGAGCTGCGGCCCTGCGGGAGCAGGAGAAGGAGGAGAAGGA
 GCGGAGGCGCGAGCGGGCCGACCGCGGGGAGGCTGAGCGGGGACGCGCGGAGCAGCGGGG
 ACGAGCTCAGGGAGGACGATGAGCCCGTCAAGAAGCGGGGACGCAAGGGCCGGGGCCGGGT
 CCCCCTCCTCCTCTGACTCCGAGCCCGAGGCCGAGCTGGAGAGAGAGGCCAAGAAATCAGC
 GAAGAAGCCGAGTCTTCAAGCACAGAGCCCCGAGGAAACCTGGCCAGAGGAGAAGAGAG
 TGGCGCCCGAGGAGAAGCAACAGCCCAAGCCCGTGAAGGTGGAGCGGACCCGGAAGCGGTCC
 GAGGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAGAAAGACCCCTCCGTGGAGGAGAAGCT
 GCAGAAGCTGCACAGTGAGATCAAGTTTGCCTTAAAGGTCGACAGCCCGGACGTGAAGAGGT
 GCCTGAATGCCCCAGAGGAGCTGGGAACCTGCGAGGTGACCTCTCAGATCTCCAGAAGAAC
 ACAGACGTGGTGCCACCTTGAAGAAGATTGCCCGTTACAAAGCGAACAAGGACGTAAATGGA
 GAAGGCAGCAGAATCTATACCCGGCTCAAGTCGCGGGTCTCGGCCCAAGATCGAGGCGCG
 TGCAGAAAGTGAACAAGGCTGGGATGGAGAAGGAGAAGGCCGAGGAGAAGCTGGCCGGGGAG
 GAGCTGGCCGGGGAGGAGGCCCCCCAGGAGAAGGGGAGGACAAGCCAGACCCGATCTCTC
 AGCCCCAGTGAATGGCGAGGCCACATCACAGAAGGGGGAGAGCGCAGAGGACAAGGAGCAG
 AGGAGGGTCGGGACTCGGAGGAGGGGCCAAGGTGTGGCTCCTCTGAAGACCTGCACGACAGC
 GTACGGGAGGGTCCCGACCTGGACAGGCCTGGGAGCGACCGGAGGAGCGGAGAGGGCACG
 GGGGAGCTCGGAGGCCCTGGACGAGGAGAGCT**TGA**AGCCGCGGGGAGCCAGGCCAGCCCCGCG
 CCGAGCTCAGGTGCCCCCTCCTTCCCGGCTCGCAGGAGAGCAGAGCAGAGAAGTGTGGG
 GAACGCTGTGCTGTTTGTATTGTTCCCTTGGGTTTTTTTTTCTGCTAATTCTGTGATT
 TCCAACCAACATGAAATGACTATAACCGGTTTTTTAATGA

FIGURE 174

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYGGKPNKRKGFNGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDDRG
VMAVTAVTATAASDRMESDSDSKSSDNSGLKRKTPALKMSVSKRARKASSDLQASVSPSE
EENSESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDSVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRRDEARRRRELEARRRREQEELRLRLREQEKEEKERRRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKS AKKPQSSSTEPARKPGQKEKRV
RPEEKQQA KPVKVERTRKRSFGFSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDS PDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEEKLAGEELAGEEAPQEKAEDKPDSTDLAPVNGEATSQKGESAEDKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLD RPGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13

FIGURE 175

GTTGGTTCTCCTGGATCTTACCTTACCACCTGCAGATCTTGGGACTCATCAGACCTCAATAATTATATAATTA
 ACACCTATTGAAAGAGAACATTGTTTTCATCAGAAAGCTAATAAGATGAAAGACTTAAGCCAGAAGCCAGA
 TTTTCACTTTTCTCGTCTTGAATGATGCTAAGCATGACCATGTGTTTCTTCCAGCTGGCCATTGGAAGCA
 AATATTCCAAAGCTCAAGTCAACCTACAAAGACTTGCCTCTTCAAAATAGCTGTATCCCTTTTGGGTCTATC
 AGAAGGACTGGATTCAAGCTCTTCTCTAGATGAGGAAAGGAGGCTGCTCTTGGGAGGCCAAGACCACAT
 CTTTCTTACTCAGTCTGGTTGACTTAAACAAAATTTTAAAGAGATTTATTGGCTCTGCAAGGAACGGGTGGA
 ATTATGTAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAAATTTATCAGAGTACTTCAGCCCTATACAA
 AACTCACATATATGTGTGGAACTGGAGCATTTATCCAAATATGTGGGTATATTGACTTTGGAGTCTACAGGA
 GGAATATTATTTCAAACTAGACACACATAAATTTGGAGTCTGGCAGACTGAAATGTCTTTTCGATCTCAGCAGCC
 TTTTGCTTCAGTAATGACAGATGAGTACCTTACTCTGGAACAGCTTCTGATTTCCTTGGCAAGATACTGCAIT
 CACTCGATCCCTTGGGCTACTCATGACCACCACTACATCAGAAGTACATTTTCAGAGCACTACTGGCTCAATGG
 AGCAAAATTTATGGAAGTTTCTTATACACAGACACCTCAAAATCCAGATGATGATAAAATATATTTCTTCTTCTG
 TGAATCATCTCAAGAGGCGAGTACCTCCGATAAAACCATCTTCTCGAGTTGGAAGAGTTTGAAGAATGATGT
 AGGAGGACAACGCGAGCTGATAAACAAGTGGAGCACTTTTCTTAAGGCCAGACTGATTGCTCAATTCCTGGAAG
 TGAATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT
 AGTATATGGAGTCTTTACTACAACAGCTCCATCTTCAAAAGGCTCTGCTGTTTGTGTATAGCATGTGACAT
 CAGAGCAGTTTTTAAATGTCATATGCTATAAGGAAAGTGACAGACCATCGTTGGGTGCATATGATGGGAGAA
 TCTTTTCCAGGGCTGGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAAGTCCACCCGAGATTTTCCAGA
 TGTATGCTCAGTTTCTATAAGCGGCACCTCTGTGATGTATAAGTCCGTACGGTCTCAGGAGGAGCAACCGTT
 CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTTCATTCAGAGAGATGGCCAGTACGA
 TGTATGTTTCTTGGAAAGACATTTGGAAGTCTTCCCAAAGTTGTACAGACTTTCCAGGAAAAGTGGAAATGGA
 AGAGGTAGTGTGAGGAGGTGCGAGATTTCAAGCACTCATCAATCATCTTGAACATGGAATGTCTCTGAAGCA
 GCAACAAATGTACATTTGGTTCGAGATGGATTTAGTTGAGCTCTCTTGCACAGATGCCACACTTATGGGAAGC
 TTGCGCAGATGTGTTCTTGGCAGAGACCCCTACTGTGCTGGGATGGAATAGCATGCTCTGATATGCTCTAC
 TTTCAAAAGGAGAGCTAGACGCAAGATGTAATAATAGGCCACCCTCAATCCAGTGTCTGGACATCGAAGACAG
 CATTAGTCAATGAACTGCTGATGAAAGCTGATTTTGGCATTTGAATTTAATCACTCTTCTGGAATGTATACC
 TAAATCCCAGCAAGCACTATAAATGGTATATCCAGAGGTCAAGGATGAGCATCGAGAGGATGGAAGCGATG
 TGAAGAAATCATCAAAACGGAATATGGGCTACTGATTCCAAGTTTGCAGAGAAGAGATTTCTGGGATGTATTCTG
 CAAGCCCAGGAGCACCTTTTATCCACCACTAGTGAAGCTGACTTTGAATGTCTTGAATGTCTTGAAGTGAACAGATGGA
 AATATCCCAGAGGGCAGAGCATGAGGAGGGGCGAGTCAAGGATCTATTGGCTGAGTCAAGCTTGAATACAAAGA
 CTACATCCAAATCCTTAGCAGCCCAAACTCAGGCTCGACCACTACTGCAAGACAGATGTGCCACAGGAGCAAGCG
 GAGACAGAGAAACAGGGGGGGCCAAAGTGGAAAGCACTGCAAGAAATGAGAGAAACGAATCGAAGACATCA
 CAGAGACCTGGATGAGTCCCTTAGAGCTGTAGCCACCTAGTTTTCTACTTAATTTAAAGAAAAGAAATTCCTTACC
 TATAAAAAATTTGCCCTCTGTTTGTATATCCCTTATAGTAATTCATAAATGCTCCCATGGAGTTTGTCTAAGG
 CACAAGACAAATAATCTGAATAGACAATATGTGATGAATATAAGAAAGGGCAAAAATTCATTTGAACAGTTTT
 CCAAGAACAAATCTTGCACAAAGCAAAGTATAAGAAATTTATCCTAAAAATAGGGGGTTTACAGTTTGAATGTCTTTA
 TGTTTTGAGTTTGGAAATTTATTTGTCATGTAATAAGTTGAGCTAAGCAAGCCCGAATTTGATAGTGATATAAGGT
 GCTTTATCCCTCGAATGTCCATTAAGCATGGAATTTACCATGCACTTGTGCTATGTTCTTATGAACAGATATAT
 CATCTCTATTGAGAAGCAGCTACCTTTGGTAGGGAATAAGAGGTGACACACAAATTAAGACAACTCCCATATC
 AACAGGAACCTTTCTCAGTGAAGCTTCACTCCTGGAGAAATGGTATAGGAATTTGAGAGGTTGCATTTTCTTCTT
 TGGCCAGTGGGTTAAATTTAGTGTACTACAACATTTGATTTACTGAAGGGCACTAATGTTTCCCCAGGATTTCT
 ATTGACTGATCAGAGTAAACAGGTTACACAGAGAGAAGTTGGTCTGTGTTTATGATGTATATACTAAT
 GCTCTACAGGGACAGAAATGCTTAAATAACTTTAATAAGATATGGGAAAATTTTAAATAAAACAAGGAAACAA
 TAATGATGATATAATGCATCTGATGGGAAGCATGCAGATGGGATTTGTTAGAAGCAAGGAAAGACAGCCAT
 AAATTTCTGCTTTGGGAAAATCATATGCCATGAAAGGAAGAAACATCACAATAAAGTGAGAGTAAATGTAA
 TGGAGCTCTTTTCACTAGGGTATATAGTAGCTGCCAATTTGTAATTCATCTGTAAAAAAATCTAGATATAACA
 AACTGCTAGCAAAATCTGAGGAACACATAAATCTCTCTGAAGAATCATAGGAAGAGTAGACATTTTATTTATAAC
 RATGATATTTTCAATATATTTTCTCTTTTAAAAAATATTTATCATCTCTGTATATTTCTTTTCTTCTG
 CTTTATCTCTCTGTTATATTTGGGTTTGTGATTATATTTGAGTGAATAGGAGAAAACAAATATAACACACAGA
 GAATTAAGAAATGACATTTCTGGGAGTGGGATATATTTGTTGAATACAGACAGAGTGTAAATTTTAAAC
 AACGGAAAGGGTAAATTAACCTTTGACATCTTCACTCAACCTTTTCTATTGCTGAGTTAACTGTGTAAT
 GTAGTATTTGTTTGTAAATTAACATAAATAAGCCTGCTACATGT

FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTyKDLLLSNSCIPFL
GSSEGLDFQTLTLLDEERGRLLLGAKDHI FLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDHHYIRTDISEHYWLNCAKFIGTFF
IPDTYNPDDDKIYFFRFRESSQEGSTSDKTI LSRVGRVCKNDVGGQSRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVVISKEKWNMEEVVLEE
LQIFKHSSII LNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCCLARDPYCAWDGNA
CSRYAPTSKRARRRQDVKYGDPI TQCWDIEDSISHETADEKVI FGI EFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERI IKTEYGLLIRSLQKKDSGMYCYCAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKKRNRHHRDLDELPRAVAT
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCTTGACCTCCCTGAGCCACACTGAGCTGGAGCCGAGAGGTCATCTGGAGCATGCCACCGGGGAGCAGA
 CAACCTCCAGGTTAAGCTGGGAGCAAGACTGAGCTGTTTCTCAGGACCTGGTGATATTTTCCCAACCCCA
 CTGACGACCTTCAGCCAGCAGGACTGATCAGGTGTGTGCTCGAGTGGGGAGCAGAAGCGCTGGCTGGCAAGA
 GTGGCTGGAGAAAGAGGTTGAGCGCTTGACCAAGCGAGCTGCCGCTGACTACAAGATCCAGAGACACTGGGCATC
 GGGTAGGCTGGGGGGGACAGGTGGCTCATGTGCACCTCTTTGCTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTGG
 AGCCATTGAGGGTGTATGGAGCTACAGAGGGGAGGGAAAGGATTTTAAGGTAAACAGTGTGGCACAATATGTTAA
 GACCAACCTTTTGGAGCTAGACCGGACATAGGTTCAAAATCTCTTCTGTGTGCTTCTAGTTCTGTAGCCCCAGGT
 AAGGGAGTGACTTAACCTCTCTGGAATCAATTTCCCTATCACTAAAGTAGGGCCAAATAATAGCACCCACCTCAT
 AGGGAAGATTAAATGACATAATGTATGTGATGCAACTAGCAAAATACCAGTCCCATAGTAAGTCAATGCCCCACAG
 TATTTCCACCCACCCCTGTCTCTGCTTCCCAACCCAGGTACTGCAACGACTGGAGCAGAGGGCGGACAGCGGCT
 CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTCGAGAGAGCATCCGCCGGGACAGGTGAGCC
 AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGAGGGGGCTGGCTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
 TGACCCAGGCGCAGGATGAGGTGGAGCAGGAGCGCGGCTCAGTGAGGCTCGGCTGTCCACAGGGGACCTCTCTC
 CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCTGCC
 CCCAAGCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTGCTATCAGGCAGGGCGTGAAGATG
 AGCTGACAAATCAGGAGGCTGAGTGGCTGGAGGTATAGAGGAGGGAGATGCTGACGAATGGTCAAGGCTCGGA
 ACCAGCACGGCGAGGTAGGCTTTGCTCCGTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCGAGGACGCC
 AAGACAGTGCAAACTCCCTGGGGGACAGGCCACAGCAATCTCGGCACAGGCCGTGACAGCTACACGGACAGCA
 GTGCAGAGGACTGAGCTTCCCTGAGGGGCACTCATCCGTCTGTGCCCGGGCCAAAGATGGAGTAGATGAGCG
 GTTCTGAGAGGGGAGATTTGGGGGGCGTGTGGGGTCTTCCCTCCCTGCTGGTGGGAAGAGTCTTCTGGCCGCC
 CAGGGCCAGCTCAACTCTTGACCTGAACAGATGCTGCGCTGCCCTCTCTCTCCAGGCTTCTCCCACTGCAAC
 CTACTCTGTGTGGATGGGCCCTGCACCTGTCTGCTGGGACAAAGCCCTGGACTTCCCTGGGTCTCTGG
 ACATGTGCACTGCACTCAGGCGGATGCTCCACCACTCCGCCGGGCTAAAGCCCGGCTACCCCGGCTGCGCAC
 CAGATCCCTCACCCTGAAGGCCAGGGAAGCTTGACCCCAAGTATGCTGCTGTCTCTATCTCAAGCTGTGAC
 CCACCACTCAATGATCCAGAGCAACACAGGCCAAAGCTGGAATGCCCTTATTTCCACCTCCTCCTCAAGGT
 GGAACCTTGCCCTTCCCAATTTCTAGAGCTGGAAGCCACTCCTTTTTCCTATGTTCTATCTCTTAGGACC
 GGAACCTACTACTCTCTCTGTCATGACCTATCTAGGGTGGTGAATGCTGAAATCTCTGGGGCTGGAAC
 ATCCCTCAAGGTCTTAGTAGTGTCTGGGCCACTCTTTCCCACTCCCTGGCTCCCATGACCCACCCACTCTGGAT
 CCAGGGTCACTGGGGTGGGGCTGGGAGAGGAACAGGCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG
 CTGTAATGGTCTGAGCGGATTTATTGACAAATGAATAAAGGCGCAAGAGGCCAGGCCAGGCGCTGGCCCTCTGTG
 CTAAGAGGGCAGGGGGCTACGGTGCTATTGCTTTAGGGGCCACACCGGGCAGGGGCTGCTCCAGCTGTGCCAC
 GCTCTATCATATGAGCGAGGTGTGGGGAAGCGGGGACAGGAGCTGTTGAGGACAGCCACCCCTGGCCCTGCCAGTGGTAG
 TGAGGGGCTGTGACTCTCTCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCT
 AGCTGGGGGCGAGTCTCTCAGTGGAGGGGAGGGCTTACGCCCCACCCACCCCTGGCCCTGCCAGCTGGTAG
 TCCATCAGCAAAATGAAGGAGACTTGAGAAAGAGGAAGATAAAGCTGTGCTTCTGTCAAGCTGTGTCCAGC
 TTTCTCCTGGGGCTCCAGGACTTCCCTACTCCACCAACCAAGGATTATGACAAAGGCTTAAGCTGCG
 AGTTTACTCTGGGGTTCAGGGAGCCGAAAGGCTTAATAGTTTAAGTAGGTGATGGGAAGTGAATTAACCTA
 TTTAGGCTCAGGAGACTCAGCTCACATACTCCCTGCTCCCTGTGTGAGAGACACTGAGAGAAAGGGGAGGG
 TCAACAAATGAGAGACAGGAGTAGGTCTATCAGTGCCCCCAGAGTAGAGAGCAATGAAGAGCCAGGCCAGTGC
 AGTCCGGCTGTGTTTCTACTGCTGATGAGAAAGTGTGCTGTTCTGGCTGCCATTTGCCCTTTGAGTGG
 CGAGCGCTGGGCTGGGCCCCCTCCCTCCGGCCCTCAGTGTGGCTGCTGCAAGAGCTGTGGGGTTCCTTTCAAGT
 CAGAGGGGTAGGCTGTGCTCCTGAGTCTCCTCATTTGATGAGGGGAGCCATCAGCGTGTCTGCGAATCCATAGCGT
 TCTCAGGGGAGGCTCTCCATGGCAGGCATCCCTGCTTGGGCTGCCCTCCCGAGACCCCTGACCCACCCCTG
 GGCTCTTCCCCACAGAGCCCACTGCTGTCTGTGGGGAGGCCATCAGCGTGTCTGCGAATCCATAGCGT
 TCTCAATGTGTGACCCGGAACCTGGGAGGGGAGGGAACACTGGGGTTAGGACCAACACTCAGAGGCTGCTGT
 GCCCTCCCTCTGACCAAGGACACTCTGAGTTTGGTGGCTACTTCCCTGAGTGGGAGGGGCTCTCTC
 AGATTGTGGGGCAACTGTGTAGCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAGGCCCACTT
 TTGGATCAGGTGCTGATCATCTGGGCCCTTACCTCAGCCCTCTTCCCTGGGACACTGCCCCACTGCCCA
 CAGAGACACAGTGGTCTCCCTCTGCGGGGGCGGCTTTTCTCTCTTGGAGCGTCCCTGACGGACAAGTGGAG
 CGCTCTTGCTGGCTGCAATGGATGCAAGGGGCTGCAAGCCAGGTGCACTGTGTGATGATGGGAGGGGCTCT
 CAGCTCGAGGCTGGAGGTGGCATCCACTGGACAGCAGGAGGAGGGGAGTGAAGGTAACTTTCCATTTCCCT
 CTATGTTTGTCTTCTTACGTTCTTTCAGCATGCTCTTAAACCCCAAGAGCCCAATTTCCCAAGCCCACTTT

FIGURE 178

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPSTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFYQAGREDELITIEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSPLESSQSDSDNPCGAEPATAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSSLVEELLGPPGPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPDGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
```

FIGURE 179A

CACAGGGAGACCCACAGACACATATGCCAGAGAGACAGAGGAGAAAGACAGAGAACAAAGGCACAGCGGAA
 GARGGCAGAGACAGGCGAGGCACAGAGCGGCCAGACAGAGTCTACAGAGGGAGCGCCAGAGAGGCTGCAGAA
 AGACACAGCGCAGGAGAGACAAAGATCCAGGAAAGGAGGCGCTCAGGAGGAGAGATTGGAGAAAGCCAGACCCCTGG
 GCACCTCTCCCAAGGCCAAGAGACTAAGTCTTCTCCATTTCCTTAACGGCTCTCAGCCCTCTGGAACATCTTGGC
 TCTGACCTTGGCAGGAGTCCAGAGCCCCAGGCTACAGAGAGGAGCTTCCAAAGGCTAGGGGTGTGGAGGACTTGGT
 GCCTTAGACGGCCTCAGTCCCTCCAGCTGCAGTACCAAGTGGCCATGTGCCCATTTGGCCGCTCTCTGGGTGTGTG
 CTTGGCAGGGCGCTGGCTGTGGGAGGCCAACCTGCTCCTGCTGCTCCCATTTGGCCGCTCTCTGGGTGTGTG
 GCTGCTTCTGCTACTGCTGGCTCTCTCCTGCCCTCAGCCGGGCTGGCCAGCCCCCTCCCCGGGAGGAGGAGAT
 CGTGTTCACAGAGAAGCTCAACCGCAGCGTCTGCTGCTGGCTCGGGCGCCCTCCAGGCTTTGTGGCCGCTTGCAG
 GGCTTTTGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAAGTTCAGGGGCTGCAGATGCAGTA
 CTTGGGCCAGGCGCCTGAGCTGCTGGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC
 GGAGTCGTTGGCATCTCTGCACTGGGATGGGGAGGCGCTGTTAGGCGTGTACAATATCGGGGGGCTGAATCCCA
 CCTCCAGCCCTGGAGGGAGGCCACCTAACTGCTGGGGGACCTGGGGCTCACATCTACGCCGGGAAGAGTCC
 TGCACAGCGTCAAGTCCCATGTCAACGTCAAGGCTCCTCTTGGAAAGCCCAAGCCCAAGCCCGAAGAGCCAA
 GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGATTCCACGGTGC
 GGGGCTTAAAGCGCTACCTGCTAACAGTGTAGTGCAGCAGCAGCCAGGCTTCAAGCACCCAAAGCATCCGCAATCC
 TGTCACTTGGTGGTACTCGGCTGATGATCTGGGGTCAGGCGAGGAGGGGCCCAAGTGGGGCCAGTCTGCG
 CCAGACCTCGGCGATTCTGTGCTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCATTTTGA
 CACAGCCATTCTGTTTACCCTCAGGACTGTGTGGAGTCTCCACTTGCACACGCTGGGCTATGGCTGTGGG
 CACCGTCTGTGAACCCGGCTCCAGGACTGTGCCATTGTGGAGGATGAGGGCTCCAGTCAAGCTTCACTGCTGCTCA
 TGAACCTGGCTATGCTTCCAGTGTCTCATGACAACTCCAAGCATGCATCAAGTGTGAATGGGCTTTGAGACAC
 CTCTCGGCATCTCTGGACCCCTGTGATGGCTCATGTGGATCTCGAGGAGCCCTGGTCCCCCTGCAGTGGCCGCTT
 CATCATGACTTCTCGGACAGGATGGCTATGGGCACTGTCTCTAGACAAACCAAGAGGCTCATGTGATCTGCTGT
 GACTTTCCTGGCAGGACTATGCTGCTGAACCGCAGTGGCAGCTGACCTTCGGGCGCGACTCCACGCATTAACA
 CAGCTGGCCGCGCTCTGTGCTGCCCTGTGGTCTCGGCCACTCAATGGCCATGCATGTGCGACAGCAATGCC
 CTGGCCCTGGGCGGATGGCACAACCTCGCGGCCGACACAGGCTGCATGGCTGGTGGTGGCTCCATCTCGCATGACCA
 GCTCCAGGACTTCAATATTCACAGGCTGGTGGCTGGGGTCTTGGGAGGAGTGGTGGTGGCTCCATCTGCTGGAGCC
 TGGGGGTGGTGTCCAGTTCTCTCCCGAGACTGCACGAGGCTGTGCCCGGAATGGTGGCACTCTCGTAGGCG
 CCGCGTACCCGCTTCGCTCTGCAACACTGAGGACTGCCAACTGGCTCAGCCCTGACCTTCCCGAGGAGCA
 GTGTGCTGCTCAACACCGCAGCGACTCTTCAAGAGCTTCCAGGGCCCATGCACTGGTCTCTGCTGCTGACAC
 AGCGCTGGCCCCCAGGACCGATGCAAACTCACTGCCAGGCCCGGCGACTGGGCTACTATGTGCTGGAGCC
 ACGGCTGGTAGATGGGACCCCTGTTCCCGGACAGCTCCTCGTCTGTGTGCGGAGGAGGAGGATGATCCATCTGTG
 CTGTGATCGCATCATTTGGCTCCAAAGAGAAGTTGACAAGTGCATGGTGTGCGGAGGAGGAGCGGTTCTGGTGTGAG
 CAAGCAGTCAGGCTCTTCAGGAAATTCAGGTACGGATACAACAATGTGGTCACTATCCCGCGGGGGCCACCA
 CATTTCTTCCGGCAGCAGGGAACCTGGCCACGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTTA
 TGCCCTCAATGGTGAATACACGCTGATGCCCTCCGCCACAGATGTGGTACTGCTGGGGCAGTCAGCTTGCCTA
 CAGCGGGGCCATCGAGCTCAGAGACACTGTCAAGCCATGGGCCACTGGCCCGCCCTTGAACACTGCAAGTCT
 AGTGGCTGGCAACCCCGAGGACACAGCCTCOGATACAGCTTCTCGTGGCCCGCCAGCCCTTCAACGCCGAGC
 CCCCATCCCGAGCACTGGCTGACCGAAGACACGATTTCTGGAGATCCTTCCGCGCGCCCTGGGCGGGCAG
 GAATTAACCTCACTATCCCGGCTGCCCTTCTGGGACCGGGGCTCGACTTAGCTGGGAGAAAGAGAGAGCTT
 CTGTTGCTGCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGGCTGAGACCTGCCCTCCTCTCTGCCCTAAT
 GCGCAGCTGGCCCTGATCGCTGTTTCTGCGCTGGGAGGCAAGTGGTTAGTGGATGGAAGGGGCTGACAGAC
 AGCCCTCCATCTAACTGCCCTCTGCCCTCGGGGTACAGAGAGGAGGGGGAAGGACAGGAGGGCTGGGCC
 CAGCTGTATTATTATTAGTATTATTCACTTTATTATGACACAGGGAAGGGAAGAGGACTAGGCTCCTGGGAA
 CCTGACCCCTGACCCCTATAGCCCTCACCTGGGGCTAGGAAATCCAGGGTGGTGGTATAGGTATAAGTGGT
 TGTGTATCGGTGTGTGTGTGTGTGAAATGTGTGTGCTTATGTATGAGTACAACTGTCTGCTTTCTTC
 TTCTCGAATTTATTTTTGGGAAAGAAAGTCAAGGCTAGGTTGGGCTTCAAGGAGTGGGATATCTTTT
 TTTTCTTTCTTTCTTTCTTTTCTTTTGTGAGACAGAAATCTCGCTTGGAGCAGGCTGGAGTGAAGTGC
 GCACATCTCGGCTCACTGCATCTCCGCTCCCGGGTCAAGTGATCTCATGCTCAGGCTCCTGAGTACGCT
 GGATTCAGGCTCTCGCCAGCCCGCCAGCTAATTTTGTGTTTGGAGACAGATCTCGTATTTGTGTC
 ACCAGGGCTGGAATGATTTCACTCACTCACTGCAACCTTGCACCACTGGGTCACGAATCTCCTCGCTCAGCTCC
 CAGTACGCTGAGATTATAGGCACTACCAACACCGCGGCTAATTTTGTATTTTATGAGAGAGGGGTTTAC
 CATGTTGGCCAGGCTGGCTCGAAGCTCCTGACCTTAGGTATCCACTCGCTTCACTCCCAAGGTCTGGGATTACAGG
 ACAGGCTGAGCCAGGCTGCTGGCCACGCCCACTAATTTTGTATTTTATGAGAGAGGTTTCACTCATGT
 TGCCAGGCTGCTCTTGAAGCTCCTGACCTCAGGTATGACCTGCTCGGCTCCCAAGGTCTGGGATTACAGG
 TGTGAGCCACCAACGCCGTACATATTTTAAATGAATTCTACTATTATGTATCTTGTGGAGTCAGACAG

FIGURE 179B

FIGURE 180

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLGAQPCLLLPVPLSWLVWLLLLLASLLPSARLASPLPREEEIV
FPEKLNGLSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGAPELLGGAEP
GTYLTGTINGDPESVASLHWDGALLGLVLQYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPNCNVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
AAKAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSSAAQTLRSFCAWQRGLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
NSKPCISLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PVTFPGKDYDADRQCQLTFGPDSTRHCPQLPPCAALWCSGHLNGLHAMCQTKHSPWADGTPCG
PAQACMGGRCLHMDQLQDFNIPOAGGWGPWGPWGDCSRTCGGGVQFSSRDCTRPVPRNGGKY
CEGRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFCSFPGPMDWVPRYTGVAPODQCK
LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPGSYALNGEYTL
MPSPTDVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSSFFVPRPT
PSTPRPTPDWLHRRQAILEILRRRPWAGRK

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**
 CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC
 AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCT
 AATTGTCCTGTTTTGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
 TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGATTACATGGAAATTGATCCTGTG
 ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
 TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAAACTCAGA
 TTAAAGTGATTCTCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
 ACAACTTTCTTTGAACAGTCAGTGATTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
 TTTTCTTAAAAATTCAAAATTTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC
 CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGAGAAGATCTTCACTTT
 CCTGCCAACGAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT
 AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTG
 AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT
 CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
 CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCC
 GCATGCTGGGGAGGGTCT**TAAT**AGGAGGTTTGAGCTCAAATGCTTAAAGTCTGGCAACATAT
 AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
 CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
 AAAAAAAAAAAAAAAAAA

FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPPKAY
DMEHTFYNSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKT
QIKVIEPFESEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSSELQDFEEEGEDLHFFPANEEKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMLEDERGYCCIIYCRGNRYCRRVCEPLLGYYPPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAAC TGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCGAGGGCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGACCA**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT
 GCTCAGCTTCTTGGGCATGGTGGGCACGTTGATCACCACCATCTGCCGCACTGGCGGAGGA
 CAGCGCACGTGGGCACCAACATCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCCGCGCCCTCATGGTCATCTCCTGCCCTGCTCTCGGGCATAGCCT
 GCGCCTGCGCCGTATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
 ACCTTTGCCATCTCTCGGCGGCACCTCTTTCATCTCTGGCCGGCCTCCTGTGCATGGTGGCCGT
 CTCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
 GGCACCTGCTTTGCCCTGTCTGCCAGGACGAGGCACCTACAGGCCCTACCAGGCCCCGCC
 CAGGGCCACCACGACCACTGCAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGTTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC
 AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
 AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATAT
 TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT
 TGGTTTGTGATCCAGGAATAAACCTTGC GGATGTGGCTGTTTATGAAAAAAAAAAAAA

FIGURE 184

MASTAVQLLGFLLSFLGMVGTLLITILPHWRRTAHVGTNILTAVSYLKGLWMECVVHSTGIY
QCQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTPAKTTFAILGGTL
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLIGGTLCLSCQ
DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:**Signal peptide:**

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 185

GAGCTCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGGCGGCAGGGCGGGCGGCCAGGATC**ATGT**CCACCACCACATGCCAAGTGGTGGCGTTCTCT
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTTT**CAGGCTT**CACCGAATGCAGGCCCTATTTCACCATCTCGGACTTCCAGC
 CATGCTGCAGGAGTGCAGGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCCTCC
 TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
 AACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
 GTCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCACAGCTAACATGTACACCG
 GCATGGGTGGGATGGTGCAGACTGTT**CAGACCAGGTACACATT**GGTGCGGCTCTGTTCTGTG
 GGTGGGTGCTGGAGGCCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG
 CCTGGCACCAGAAGAAACCACTACAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTC
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAACAAGAG
 ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA
 TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGAGAGCTACCCAAAAA
 AACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTC
 ACCATAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
 TTCTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCAC
 ATTTTGATGATTTAGACAGACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTA
 TTTCCAGCTTATCCCCAAGAAAACCTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT
 CTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGCTAGTAATAAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG
 TGATCTTAAAGTTACCAAACCAAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTG
 CTGTTGACATCTTCTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG
 TCCTCTTTCTGTGCGGGGTGAGAAATGTCCCTAGATGAATGAGAAAAATTATTTTTTTAAT
 TTAAGTCCTAAATATAGTTAAATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGA
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTTGACATTGTCT
 ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCAGAAAGTTCGAGACTAGCCTG
 GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG
 GCATACACCTGTAGTCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCAGGG
 AGGTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
 TCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCTAGGAAGTAGGTTAA
 ACTAATTCTTTAA

FIGURE 186

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTC CG
 GAGTCCAGCTGGCTAAAACTCATCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG
 GGCTGTTTCTTGGTGGTGTGGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG
 AGAGTGTGCGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGTAACATCAGGATGCAGTGCAAAATCTATGATTCCTGCTGG
 CTCCTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC
 TTGGCTTTTCATGATGGCCATCCTTGGCATGAAATGCACCAAGGTGCACGGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGGTGGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
 GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCCT
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA
 GATACTCGATACCTTCCCATCGCACACCCAAAAAGTTATCACACCGGAAAGAAGTCACCG
 AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGC
 CATGCAAAATGACAAAAATCTATTAATTCTCTCAAAATGGACCCCAAGAAACTTTTGATTTA
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAACGTGTCATCAGTATTATGATTCTATAA
 GCTATTTACGAGAATGAGATATTAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTACTTCAAAATGACATTGCT
 AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCTCCATTATATAATGA
 AGATTAAATGAAGGCTTAAATCAGCATTGTAAGGAAATGAATGGCTTCTGATATGCTG
 TTTTTTAGCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTT
 TTCTTGTTGATTAAATTAACATTTTTTAAACGCAGATATTTTGTCAAGGGGCTTGTGATTCA
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
 GTTTTAGGAAAGTGAAAAATTTTTGTTTTGTATTGAAGAAGAATGATGCATTTTGACAA
 GAAATCATATATGTATGGATATATTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
 AATATAAATAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTGTCTACCAAAAAACAACA
 ACAAAAAAGTTGTCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATG
 TCATTTTTGTCTGTGAAAAATAAATTCCTTCTGTGACCATTTCTGTTAGTTTTACTAAA
 ATCTGTAATACTGTATTTTTCTGTATTATCCAAATTTGATGAACTGACAATCCAATTTGA
 AAGTTTGTGTCGAGCTGTGTAGCTTAAATGAATGTGTTCTATTGCTTTATACATTTATA
 TTAATAAATGTACATTTTTCTAATT

FIGURE 188

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVMPQWRVSAFIENNIIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLALLSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCCATGGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGGCTGGGTG
 AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
 CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCTGCGTGGTGCAGAGCACC GGCC
 AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
 GCCCTCTGTGTCACTCGCCCTCCTTGTGGCCCTGTTGCGCTTGCTGGTCTACCTTGCTGGGGC
 CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGCCCCGCTGGTGTACCTCTGGGA
 TTGTCTTTGTCACTCAGGGGTCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC
 ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCTCCCT
 CTA CTGGGCTGGGGGCCTCAGGCCTTTTGTGTGGTGGGGGGTGTGTGTGTGCACCT
 GCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCC
 GCCATCTCTCGGGGGCCTCTGAGTACCTACCAAGAATTACGTCTTGACGTGGAGGGGAATG
 GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGT
 CGTACCTTTTGTCTTGCCCTCCTGCTATTTTCTTTTGACTGAGGATATTTAAATTCATTT
 GAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCCTTGG
 ATGATGGAGCCAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCATCTTAGAAGC
 CAGTCAAGCTATGGAACATAATGCGGAGGCTGCTTGTGTGCTGGCTTTGCAACAAGACAGAC
 TGTCCCCAAGAGTTCCTGCTGCTGCTGGGGCTGGGCTTCCTTAGATGTCACTGGACAGCTG
 CCCCCATCCTACTCAGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAAATCATCTG
 TTAACAAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTTCTCCGCTCCTGATAAGACG
 TCCACCCCCAGGGCCAGGTCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
 CTTCTGCCCTGCCCCCTCGTCTACCCCTTTACACTCACATTTTTATCAAATAAAGCATG
 TTTTGTAGTGCA

FIGURE 190

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIVVAQVVWEGGLWMSCVVQSTGQM
QCKVYDSSLALPQDLQAARALCVIALLLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLPVCWTAHAIIIRDFYNPLVAEAQKREL GASLYLGWAASGLLLLGGGLLCCTCP
SGGSQGQPSHYMARYSTSAPAI SRGPSEYPTKNYV
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Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG
 AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTTTATCCC
 TTGCAAATTGCTGGGCTGGTTCTTGGGTTCCTTGGCATGGTGGGGACTCTTGCCACAACCTT
 TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC
 TGGGAAGGGCTCTGGATGAAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
 TAGTCTCTTGTGGCTCTCCCGCTGCCCTGGAACAGCCCGGGCCCTCATGTGTGTGGCTG
 TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGACACA
 GGCTCTAACGAGAGGGGCCAAAGCATACCTTCTGGGAACCTTCAGGAGTCTCTTCATCCTGAC
 GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA
 ACCGAGCCATCCACATAGGTGAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA
 AGCGCTGCTGCTCTTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGTGCTGCAACAGAAA
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACAGATAAGCGAAGAA
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTTGCTCCAAGT
 ATGGACTATGGTCAATGTTTTTTATAAAGTCTGTAGAACTGTAAGTATGTGAGGCAGGA
 GAATCTGCTTTATGTCTAGATTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG
 AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAATGCATTGACTATTGTTG
 GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG
 TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA
 GTTGAATTGATATTCTATAACAATAAACATATACCTATTCTA

FIGURE 192

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV
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Important features of the protein:**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGC**ATGA**AAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA
CATACCTACCAGTTTGTGGTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGC**TAA**ATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTAGAGTAATCTTG
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCAGA

FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLCTVVYFCSSSEASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC

Signal peptide:

amino acids 1-19

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC
CGCCGCC**ATG**GCTGCCTCCCCGCGCGGCCTGCTGTCTGGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTCAA
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA
ATTCCCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCGAGGTGC
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACT**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAATAGCGATTC
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTACAGCAGAT
CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAACAAACACATGTAAATGCCTTT
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

FIGURE 196

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKCLKMLQKREAPVPTKTKVAVDENKAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDDYYQRHYD
EDSAIGPRSPYGFRRHGASVNYDDY

Signal peptide:

amino acids 1-30

FIGURE 197

CGGCTCGAGCCCCGCCGAAGTCCCCGAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC
GGTAGCGCGGCGGGCAAGGCAGGCGCC**ATG**ACCTTGATTGAAGGGGTGGGTGATGAGGTGAC
CGTCTCTTTCTCGGTGCTTGCTGCTTCTGGTGCTGGCCCTTGCTGGGTCTCAACGCACA
CCGCTGAGGGCGGGACCCACTGCCCCAGCCGTCAGGGACCCCAACGCCATCCAGGCCAGC
GCAGCCATGCGAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCGACCT
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTACAGCAACACCGCCAG
CCCCGGACTCCCCGCGAGGAGCCCCCTCGTGCTACGGCTGAAATTCCTCAATGATTACAGAGCAG
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTGAAAAGGACCCAGTTTCCCGGCCG
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGG
GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCCGTCCC
CCAAATCCCCCTGCCCGCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAAATCGGCAGCCT
GCTGCTGCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
CCTTCTTTCCCTGACCGCCACTCTGGGCTGGCCGGCTTACCTGCTCCTCAGTCTCCTG
GCCTTTGCCATGTACCGCC**GTAG**TGCCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTCC
GGACCTTGCTCCCCGCGCCGCGCGGGAGCTGCTGCCTGCCAGGCCCGCTCTCCGGCCTG
CCTCTTCCGCTGCCCTGGAGCCAGCCCTGCGCCGAGAGGACTCCCGGGACTGCGCGGAGG
CCCCGCCCTGCGACCGCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA
CTGGGAGTGGGCTCCTCGGGGTGCGGCATCTGCTGTCGCTGCCTCGGCCCCGGGCAGAGCCG
GGCCGCCCGGGGGCCGCTCTTAGTGTTCTGCCGAGGACCCAGCCGCTCCAATCCCTGAC
AGCTCCTTGGGCTGAGTTGGGACGCCAGGTCGGTGGGAGGCTGGTGAAGGGGAGCGGGAG
GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTAAAAAAAAA
AAAAAAA

FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPNCVLHCHVSTRVGPPNPPCPPGS
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

FIGURE 199

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCC
TCAGCTGCACCTCTCCCTCCAAGGATGACAAAGGCCTACTCATCTAATTGGTTCAGCAGC
TTTCTTGGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT
GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG
AAAGCAAGTTCAACATATCAAAGATAAATGAAAAATGCGGATGGAAGCTTTGACTATGGCCTC
TTCAGATCAACAGCCACTACTGGTGAACAGATTATAAGAGTTACTCGGAAAACCTTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAAGGCATCCACTGCGCAAAAAGGA
TTGTGTCCGGAGCACGGGGGATGAACAACTGGGTAGAATGGAGGTTCAGTGTTCAGGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGATGTAACAGGGTGGCGGTGCACCGTGG
AGTCATTCCAAGACTCTGTCTCTCACTCAGGGATTCTTCATTTCTTCTTCTACTGCCTCCA
CTTCATCTGTATTCTTCTTCTTCCATTACAACATAAACTGACCAAGAGCCCCAGGAATAAA
TTGGTTTCTTGGCTTCCCTCTTCACTCCATCCCATCTGGACCAAGTCCCGTGTTCTGTCTGTTAT
TTGTAAACTGAGGACCACAATAAGAAATCTTTATATTATCG

FIGURE 200

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSENLCVDCQDLLNPNLLAGIHC AKRIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTGACGCCCTGCTTGACTGAGAACCCA
 CCAGCTCATCCAGACACCTCATAGCAACCTATTATACAAAGGGGGGAAAGAAACCTGAG
 CAGAATGGAATCATTATTTTTTCCCAAGGAGAAAAACCGGGGTAAAGGGAGGGAAGCAATTC
 AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAGAAATCCACTCAGAGAGGAC
 TTGGGGTGAACCTTGGGTCTGTGGTTTTCTGATTGTAAGTGGAGCAGGCTTGCACACGC
 TGTGGCAAAATGTCAGGACAGGTTAAGTGACTGGCAGAAAAACTTCCAGGTGGAACAAGCA
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTTAACCTGAACATGAC
 CTGTGCTATTTGGCAAGTTCTAGCAACATGCTCCTTAAGGAAGCATACAGGCACAGACCATG
 CAGACTCCAGTTCTCTGCTGCTCCTGATGCTGGGATGCGTCTGATGATGGTGGCGCATGT
 TGCACCCCTCCCCACCACACCTTGCACCAGACTGTACAGCCCCAAGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCTGCCACCCCTTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCCGTGGCCCTTACCCAGGGCCAGAAGGAACAGAGCCAGGGCAGGAGAGGTGGG
 AGCTACCGCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG
 GGCTGATGAGGACGGGAGGTTGTCTGAAGAAGAGGAGTTGACCCCGTTTACGCTGGACCCAC
 GTGGCCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTTGCCCGAGGTGCGG
 CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCCCAGCCAGCGTTCATCTCTG
 TTTCCATGATAGGCCCTGGTCCACTCTCTGCGGACTGTACACAGCATCTCGACACAGTGC
 CCAGGGCCTTCTTGAAGGAGATCATCTCTGTTGACGACCTCAGCCAGCAAGGACAACCTCAAG
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGTGAAGTTACTCAGGAGCAACAAGAG
 GCTGGGTGCCATCAGGGCCCCGGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT
 TCATGGATGCCCACTGCGAGTGGCACCAGGCTGGCTGGAGCCCTCTCAGCAGAATAGCT
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA
 TTACCCCTCAAAGCACTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCTGCGGAAC
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG
 GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC
 TCTTATGTCGCTGCGAGGTGGTGAACCTCGAAGTGTCTTCAAGGCTGCTCTGTGGTG
 GCTCTGTTGAAATCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTTCCCAT
 TCCCCCTCAGCCAGGAGGCCACCTGAGGAACAGGGTTCGATTGCTGAGACCTGGCTGGG
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCAGAGGCTTCTCCTTGAGCAAGGCTGAGA
 AGCCAGACTGCATGGAACGCTTGCAGCTGCAAGGAGACTGGGTGTGCGACATTCCACTGG
 TTTCTGGTAAATGTCTACCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAAA
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCTGGGCT
 GTCCCATGGTGTGGCTCCTTGCAAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACAGC
 AGGAAGGAGATTCACTTTGGCAGCCCCAGCACCTGTGCTTTGCTGTCAAGCAGGACAGGT
 GATTTCTCAGAAGCTGCAGGAGGAAGGCTTGGCCATCCACCAGCAGCATGGGACTTCCAGG
 AGAATGGGATGATTTCTTCCATCTTTCTGGGAAATGCATGGAAGCTGTGGTGAAGAAAAAC
 AATAAAGATTGTACCTGCGTCCGTGTGATGGAAAAGCCCGCAGTGGGCGGCTTTGACCA
 GATAAATGCTGTGGATGAACGATGAATGTCAATGTGAGAAGGAAAAGAGAAATTTGGCCATC
 AAAATCCAGCTCCAACTGAACGTAAAGAGCTTATATATTTCAATGAAGCTGATCCTTTGTGT
 GTGTGCTCCTTGTGTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTTCTCCTTT
 TCACACCTTATTTCAATTGACTGCTGGCTGCTTA

FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG
ESQDVWLEAEDEGESEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR
RQDKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLFVMDAHCECHPGWLEPLLSRIAGDRSRVVS
VIDVIDWKTFOYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQNDSDSHSPLDQEATL
RNRVRIAETWLGSEFKETFYKHSPEAFSLSKAEKPCMERLQLQRRLCGRTFHWFANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCAVVRQEQVILQNCTEEGLAIHQHWDFFQENGMIHVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGACA**ATGGA**
 GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC
 TGCCCTCCCACCGCCTGCTCAGGGCTCTTCATCCTCCCTCGAACCCACCAAGCCCCAGCC
 CGCCCCCGTGTGCCAGGGGAGGCCCTCGGCCACGTCATGTGTGCGTGTGGGAGCGAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTCGGCAAGTCTGCCTGGCATTG
 CACCCCAAGCCACCCATCAGGCTTTGAGGAGGGGCGCCCTCATCCCAATACCCCTGGGCT
 ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG
 ATTTCTGGACTATGGTTTGTGACGCCCTCATGGGCTCGAACCCCAACCCCACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCCCTGCGGCCATT
 CTGTTGCGGGGCGGTGGGGAAGGTGTGGACCCCAAGCTCTATGTACAATTACCATTCTCCAT
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC
 GACGCAGACCCTCAGGGCAGCAAGGTGCCCTGAGGAGGAGGAGGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCTTCGGGGACTCACCTACCCCAACCC
 TGACCATGAGGAGCCCCGAGGGGACCCCGGCTGGGATGCCCCACCCCAAGGGGCTCCAG
 CCTTCCAGTTGAACCGT**TGA**GGGGCAGGGGCAATGGGATGGGAGGGCAAAAGAGGGCAAGC
 TTAGTCTTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGTAGTGAGGAGGCAGGCGTGGC
 CTCCACAGCCCCCTGGCCCTCCCAAGGGGCTGGACAGCTCCTCTCTGGGAGGCACCCCTT
 CTCTCCCAGTCTCTCAGGATCTGTGTCTATTCTCTGCTGCCCCATAACTCCAACCTCTGCC
 TCTTTGGTTTTTTCTCATGCCACCTTGTCTAAGACAACCTGCCCCCTTTAACCTTGATTCC
 CCTCTTTGTCTTGAACCTCCCTTCTATTCTGGCCTACCCCTTGGTCTCTGACTGTGCCCTT
 TCCCTCTTCTCTCAGGATTCCTTGGTGAATCTGTGATGCCCCCAATGTTGGGGTGCAGCC
 AAGCAGGAGGGCAAGGGGCGGCACAGCCCCATCCCACTGAGGGTGGGGCTGCTGGGGA
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCTTGACACCAACCCGGAAACATCCCCAGCC
 CCACGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCTGCATATCTGTGACTTCG
 GGTCCCTGTCCCCACCCTTGTGCACTCACATGAAAGCCTTGCACTACCTCCACCTTCAC
 AGGCCATTTGCACAGCTCCTGCACCCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCACATTTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTTCTGCACTTTACCTCTCATGTGCGTTTTCCCGGCTGATGTTGTGGTGTG
 TGTGCGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACTCGTTTCCGCGAGCCCTGC
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGCTCCTTGGGCCCTCATCGGTGATGG
 TCTCGTCCCATTCCACACCAATTTGTTTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA
 TCACCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCAAGACTTCACCCCAAGCCCA
 CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCTGCTGCACTACATGAGAA
 AGGGACTCCCATTGGCCCTTCCCTTCTCCTACAGTCCCTTTTGTCTGTCTGTCTGGCTG
 TCTGTGTGTGGCCATTCTCTGGACTTCAGAGCCCTGAGCCAGTCCCTCCCTTCCAGCCT
 CCTTTGGGCTCCTCACTCACTTAGGCTGCCAGGACCGGAGTCAGTGGTTTCAAGGCT
 ATCGGAGCTCTGCCTCCAAGTCTACCCTTCCCTTCCGGACTCCCTCTGTGCCCTCCTTT
 CCTCCCTCCTTCTTCACTCTCCTTCTTTTGTCTCCCTGCCCTTCCCCCTCCTCAGGTT
 CTTCCCTCCTTCTACATGGTTTTTCCACCTTCTCCTTCCCTTCTTCCCTGGCTCCTAGGCT
 GTGATATATATTTTTGTATTATCTCTTCTTCTGTGGTATCATCTTGAAATTACTGTG
 GGATGTAAGTTTCAAATTTTCAAATAAAGCCTTTGCAAGATAA

FIGURE 204

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKEGECLEESWTNPYKQCSWSSLNYGIDLKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCGCTGCCCTCACTCCCGGCCAGG**ATG**G
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
GTCGGGAGAAGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTCGCTGGGGCCCGGCCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
CGTGGTGTGGCGCTCGTGGTCGTGCGCTGAGAAAGTTTTCTGCCTCC**TGA**AGCGAATAAA
GGGGCCGCGCCCGGCCGCGCGCGACTCGGCAAAAAAAAAAAAAA

FIGURE 206

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVVESTSPGREPVDTG
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCCGTTGGTTGGTGC GCGGCTGAAGGGTGTGGCGCAGCAGCGTCGTTGGTTGGCCGGCGG
 CGGGCCGGGACGGGC **ATG**GCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA
 CGGCTGTCTGCAC TGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
 ACTTCAAGTCTGCTGGTGGGTGGGCGACATCCCCGTGT CAGGGGCGCTGCTCACC GACTGGAGC
 GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACC CGGGAGAAGCTGGA
 CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
 CCGGGTATTTCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
 GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGGGGACCTCCCC **TAA**GTAGCCC
 CCAGAGGCGCTGGGAGTGTGCCACCGCCCTCCCTGAAGTTTGCTCCATCTCAGCTGGGG
 GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAAC CAGGCCGAT
 CGACTGT CAGCACCCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAAC TGACAG
 ACTCGACGTGCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCACCCGT
 GCCAGGGCCCTACTGTCCCTGGGGTCC CAGGCTCTCCTTGAGGGGGCTCCCCGCTTCCAC
 CTGGCTGTATCGGGTAGGGCGGGCCGTGGGTT CAGGGGCGCACCACTTCCAAGCCTGTGT
 CCCACAGGTCTCGGCGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACACATAAATAAC
 TGGCACAAGTAAGTCCCCCTCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG
 GGTGAGTATGTGTGGGCGACAGGCTGGCTCCCTCAGCTCCCACGTCCTAGAGGGGCTCCCGA
 GGAGGTGGAACCTCAACCAGCTCTGCGCAGGAGGCGGCTGCAGTCTTTTCTCCCTCAAAG
 GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTCCCTAAAGGGTCCCCATAGGGTCTGGTTCC
 ACCCATCCAGGTCTGTGGTCAGAGCCTGGGAGGGTCCCTACGATGGTTAGGGGTGCCCC
 ATGGAGGGGCTGACTGCCCCACATTGCCTTT CAGACAGGACACGAGCATGAGGTAAGCCGC
 CCTGACCTGGACTTCAGGGGGAGGGGGTAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT
 AGATCAGTGGGGCAGCTGCAGGTGGGGCTCTCCTATACCTGGGACACCTGCTGGATGTCAC
 CTCTGCAACCACCCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCCTTCTCCTGG
 CCTGGGACACACAGACCACCCCGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA
 AGGGGTGCTCGTAAGCCAAACACAGCGTGCCGCGGCCTGCACACCCTTCGGACATCC CAGGC
 ACGAGGTGTCTGGATGTGGCCACACATAGGACACACGTC CAGCTGGGAGGAGAGGCCT
 GGGGCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
 CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT
 TGAAGATGCTGCTGAGTGTCTAAGCAGCACTGACAGCAGCTGGGCCTGCCCAGGGCAAC
 GTGGGGCGGAGACTCAGCTGGACAGCCCCTGCTGTCACTCTGGAGCTGGGCTGCTGCTGC
 CTCAGGACCCCTCTCCGACCCGACAGAGCTGAGCTGGCCAGGGCCAGGAGGCGGGAGG
 GAGGGAATGGGGTGGGTGTGCGCAGCATCAGCGCCTGGGCAGGTC CGCAGAGCTGCGGGA
 TGTGATTAAAGTCCCTGATGTTTCTC

FIGURE 208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMMQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP

Signal peptide:

amino acids 1-15

FIGURE 209

AGCAGGAGCAGGAGAGGGACAA**ATG**GAAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCTTG
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC
 ACTGAGGTGGCTGTCTAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATATCCCA
 TAGCATGGTGCAAAAATTTCCAGGCGTGTCATTTGGGATCAGCACTGATTTCTGAGGTTCTGA
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTTCGCTGGTAGACAATGAACAAC TG
 AATTTAGAGGACGAAACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCGTGTACTGTGATTGGGTTATTCAACAGCG
 TAATTCAGATTCTCTCTCTGATAATGAACAAGGCCTCCCCAGGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG
 TGGTATGAAAGAAAAATGGGAAGGTGATATCATTTTTCAAACATAAGGAGTCTCAACTGCCAG
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATCACTGCCACAGCAGAAGTTTCC
 GTAGAGCATGTGCAAACTTTTGTGATGGATTCTTAAGTGGAAAAATTGTTGAAAGAAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAACTCT**GTA**CTTCTCCTTGGAACACATATGGCC
 AAGTATCTACTTTATGCAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCTGCCAACACACACACACGACGTGCACACACGACGACGCGTGCACAC
 ACACACGCGCACACACACACACACAGAGCTTCATTTCTGTCTTAAAAATCTCGTTTTCTC
 TTCTTCTTCTTTTAAATTTATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTTAGAGAAAGATTGTTCCAATTTGTCAATTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCTTGCTCTTTTAAGGTTACCTAAGGGT
 TGAAACTCTACCTTCTTTTCATAAGCATGTCCGTCTCTGACTCAGGATCAAAAACCAAGG
 ATGGTTTTAAACACCTTTGTGAAATTGTCTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACCTCAGCAGAAATAGACCATGTGAAAACCTCATGCTTGGTTAGCATCTCCAACCTCC
 TATGTAAATCAACAACCTGCATAATAATAAAAGGCAATCATGTTATA

FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRDVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMTYENPVTVIGLFNSVIQIHLILLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDWDTLPTAEVSVVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGAGCGCGCGTGGAGGTGCCACCCGGCGCGGGTG
 GCGGAGAGATCAGAAGCCTCTTCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
 GACGCGGCGGCGGCGGCGGCTGCTGAGTGGCTGGACG**ATGG**CAGCGTCCGCCGAGCCGGG
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTGTGGCGGCGGCGCTTGG
 GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA
 ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
 TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCTGTTTTTCCACTACTC
 CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC
 TATATCTGTGATGTCAAAAACCTCCTGACATCGTTGTCCAGCCTGGACATTAGGCTCTA
 TGTCTGTAGAAAAGAGAAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
 CTGTGGTCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA
 AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTACCAGTTAAGCAGGC
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC
 AGGGCCCAAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC
 AAGTCAGAGTCTGTGGTGATGCGGATATCCGAAAGAAT**TAA**GAGAATACCTAGAACATATC
 CTCAGCAAGAAACAAAACCAAACTGGACTCTCGTGCAGAAAATGTAGCCATTACCACATGT
 AGCCTTGGAGACCCAGGCAAGGACAAGTACAGTGTACTCACAGAGGGAGAGAAAAGATGTGT
 ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA
 TGAAGATGGTATGATTCTACATATGTACCATTTGTCTGTCTTTTGTACTTTCTTTTC
 AGGTCATTTACAATTGGGAGATTTGAGAAACATTCCTTTCACCATCATTTAGAAATGGTTTG
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG
 GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
 GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTATTTGTCTGCCGCTTTTAAAA
 AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT
 AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG
 AAATGTGTCATATCAATTTCTGGATTATAATAGCAAGATTAGCAAGGATAAATGCCGAAG
 GTCACCTTCACTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAAATCCAAGCTTTGCTT
 GAGAAGTTTTGTAACTGGAGAGTAAAAAGTATCGGTTTTTA

FIGURE 212

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKSDASINIEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGCTSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGQPVIIYAQLDHSG
GHHSDKINKSESVVYADIRKN

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGTGCAGCAGTGACTGCCCGGGCTGCCGCC
 CCCGGGGGCTTGGCCTCAAGTGCGGACGACGCGGGTCCATCAGCGCGCCGGGCTGCCGCC
 TCTCGGCCACGGCTGGTTCGGGGGCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC
 TGGCAGGTGGGCTGAGGGGCGCGGCCCGCGCAGTCCCCGCGGCCCCGACCTGAGGCG
 TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCGTGGTCTCCGCAGACCCGGC
 GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGAAAAAGAAGTC
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG
 CAGGGAAACTGGATCTTGATATTCAGTACAACATTATGTTCCGAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGAATTCTG
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTGAAGATGA
 TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTT
 ACTAAATTTAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATCAAACCTGGCAAGAA
 AAAGAATGATTTTGAACAAGCGAATTATATTTGAGAGAAAAGTTGAAAATTCAATTGAAT
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA
 ACTTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTGGA
 CTATATGCAGAAAATATTCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
 CAGTGATTTACAATAGAGCAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC
 TTAACACTATTTTATTAATTAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC
 CACATTTTGGGAGCTTTTCTACATGTCTGTTTCTCATCTGTAAAGTGAAGGAAGTAAACA
 TGTTTATAAGTAAAAAA

FIGURE 214

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQESLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVCKPETVMRIASISKSITMVALAKLWEACKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFTEQENEAKCRNSKPGKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRRAR
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG
 AGGCTGGTGGGAAGAAGCCGAG**ATG**GCGGCAGCCAGCGCTGGGGCAACCCGGTGCTCCTGC
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGCAGCGGCTGCCGGGCCGGGACT
 GGTGCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCGCTGTGGCACGGTGGGGCTGCT
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
 TGGAGTCGCACCTGTCCGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
 GTGTCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCAAGGAGCAGAAG
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCTGTCGCTGTTTCCTCATGATGT CAGG
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC
 TTTGCTGTGTGCCACCCTCCCTG**TAA**GTCTATTTAAAAACATCGACGATACATTGAAATGTG
 TGAACGTTTTTAAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG
 TCCTGATGTACAAGCTTGATTGAAATTCAGTCTCACTTGATACGTTATT CAGAAACCCAAG
 GAATGGCTGTCCCCATCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT
 TAAACTGTCCCCAGATCGACACGCAAAAAAAAAA

FIGURE 216

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEEERGRLRDVAALNGLYRVRIIPRRPGALDGLEA
GGYVSSFVPACSLVESHLSDQITLHVVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWYIIPVVLFLMMSGAPDTGGQ
GGGGGGGGGGSGLCVPPSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT
 GGAGCCGGACGTGTCCGGGGCGTCCCGCAGACCGGGGCAGCAGGTCTGTCGGGGGGCCACC
ATGCTGGTGA CTGCTACCTTGTCTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAAC T
 GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTTCTTGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
 CTCTATAAACTCTACCAGCATTA CTACTTCCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
 TGGCCTTGCTCTACAGTCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC
 GCAAGAATTCTTGTGTCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAA CTCTCT
 CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT
 GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGCCCTGTAGCGCCCTTTGTGGCTGC
 CATCCCTCTCCTGGCTCTGGCAGGGGCCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC
 GGCAGCGTGCCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCCTCCTGTGCGACCGCCGC
 GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTCATCTTCATCTTTGTCTTCCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGCTGTCCCTTGTGCTGCTCATCGTCGTCTTCTCTCTTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTTCATAGCCTTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCTTAGGGCT
 CCTTGTCCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTACAGCATTTGCTCTG
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTCACCGTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGGACAGACTCTTGAATCCAGCTATCCGGGATGTACAGATCTCTCTGT
 GACTGACTTTGTGACTGTCCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA
 TGGGGGTGATGGA CTGGAAGAAGGTGCCAAAAGTTCCTCTGTGTACTCCCATTTAGAAA
 ATAAACACTTTTAAATGATCAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDIFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
VLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFFSSFMAASLLGSSLYRIATSKRYHLQ
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPMSFLRRKVIPET
EQAGVLNWFVRVPLHSLACLGLLVLHSDRKTGTRNMFSCSAVMVMALLAVVGLFTVVRHDA
ELRVPSPTTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGGGGGCGGCGAGAGGAAACGCGGCGCGGGGCCGGCCCTGGAG**ATG**
 GTCCCCGCGCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCCTCGCGGCCA
 CGGCTTCCGTATCCATGATTATTTGTAAGTCTGAGTCTGGGGACATTCGATACA
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
 CACCTTGTCCCCGCTGAACCTCCAGAGGCTGCGGGGAACTCAGCAACGGTTTCTTCATCCA
 GGACCAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCC
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCACTTGACAATGACAGCTTCTAC
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTGCTCGG
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
 CCATCCCAGTCAATGTCAACAGCATCCCCACCTTTGAGCTGCTGCAACGCCCTGGACCTTC
 TGG**TAGA**AGAGTTTGTCCACATTCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
 AGGAATTTTGTACTTGGGAATTTGGAGATAGCATCTGGGACAAGTGGAGCCAGGTAGAGGA
 AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGAAGCCACACCACTGGCCTTCCCTTCCCAGG
 GCCCCAAGGGTGTCTCATGCTACAAGAAGAGCAAGAGACAGGCCCAAGGGCTTCTGGCTA
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACT
 CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
 AGTGGTTTAAAGAGCTGGTGTGGGGACTCAATAAACCCCTCACTGACTTTTTCAGCAATAAA
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFFGIFHTRYEQ
IHLVPAEPPEACGELSNQFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVVISDNAVNDNSF
YVEMIQDSTQRTADIPALFLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

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Signal peptide:

amino acids 1-20

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FIGURE 221

FIGURE 222

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCgiYKDNNKSSIHCMdLSQRYCLMAVFNViyLENEdSE
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCTTCTGGATGGGGGGCCAGGGGGCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAACCAGACGCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTTACAGCACCCTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGCTGTAGGTCTTCTCCTGGTGAAAAGTGTCAGGTGAAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTTGTCGCCTTCCAAGCTTCTCCGGGTATGGTCATGTACACCAGCAA
GGACCCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAAGTTAATCTCACATACTC
AGCAAACCTACCCGTGGGTCGC**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAACAGAGTCGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAAA

FIGURE 224

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVVK
LGDSWDVKLGALGGNTQEVTLQPGEYITKVFAFQAFLRGMVMTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

Signal peptide:

amino acids 1-22

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAACCTGGGTGCTCATACGGGAACCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAATTGGCTGGAAGAATACATCATGTTTTTCGATAAGAGAAATTTAGGATCCAGTT
 TTTTTTTTAAACCGCCCCCTCCCACCCCCAAAAAACTGTAAAGATGCAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT
 TATTTTGTCTTGGAGTGTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
 CCCAAGGGGTCCAATTTTTCTTCCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTG
 ACAGGGGCTGTATGCAACTGGCCCCTAAGCCAAAGCAAAAGACCTTAAGGACGACCTTTGAA
 CAATACAAAGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCACTGTCTTACTGACAAATGCTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGGCCAAATGTTATTTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA
 TATCTGCTGGTGTCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTTAAGTATAAT
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT
 TGACGAAAATGCTTTTAAATGGAATACGACAGCTCAAAGAGCTGATTCCTTAGTTTCCAAAGAA
 TCTCCTATTTTCTTAAACAATACCTTCAGACCTGTGACAAATTACGGAACCTTGGATCTGTCC
 TATAATCAGCTGCATTCTCTGGGATCTGACAGCTTTCGGGGCTTGCGGAAGCTGCTGAGTTT
 ACATTTACGGTCTAATCCCTGAGAACCATCCCTGTGCGAATATTTCCAAGACTGCCGCAACC
 TGGAACTTTTGGACCTGGGATATAACCGGATCCGGAAGTTTAGCCAGGAATGCTTTGCTGGC
 ATGATCAGACTCAAAGAAGTTTACCTGGAGCACAATCAATTTTCCAGCTCAACCTGGCCCT
 TTTTCCAAGGTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAAATAAAATCAGTGTCATAG
 GACAGACCATGTCTGGACCTGGAGCTCCTTACAAGGGCTTGATTTATCAGGCAATGAGATC
 GAAGCTTTTCACTGGACCCAGTGTCTTCCAGTGTGTCGGAATCTGCAGCGCTCAACCTGGA
 TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA
 TCAGTCTTGTGGGAATATATGGGAATGCAGCAGAAATTTTGTCTCCCTTGTAACCTGGCTG
 AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTTATCTGTGCCAGTCCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAGTACTACAGAGAGGT
 TTGATCTGCGCCAGGGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCAT
 GAGAGCAAAACCCCTTTGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC
 TGACGCCGAGACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG
 TGCTCGTCATCTGCTGGTTATCTACGTGTATGGAAGCGGTACCTTGCAGCATGAAGCAG
 CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAT
 GACTCCCAGCACCCAGGAATTTTATGTAGATTATAAACCCCAACACGCGAGACACGCGAGA
 TGCTGTGTAATGGGAGGGGACCTTGCACCTATAACAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAGAGCTCTTAAAGCTGGGAAATAAGTGGTGTCTTATTGAACCT
 TGGTACTATCAAGGGAACGCGATGCCCCCTCCCTTCCCTCTCCCTCTCACCTTGGTGG
 CAAGATCCTTCTTGTCCGTTTTAGTGCATTATAATACTGGTCATTTCTCTCATACATA
 ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAACCTCCGGTTTAAATATA
 TACCTATTGTATAAGACCTTTACTGATTCATTAATGTGCGATTGTTTTAAGATAAAACT
 TCTTTCATAGTTAAAAAATAA

FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTLLTMLSSAERGCPKGCRCCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRLNLDLSYNQLHSLGSEQFRGLRKLKLSLHLRSNSLRTIPVRIFQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKLHLHLEHNQFSKLNALFPRLVSLQNLQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLSFKGLRENTIIICASPKEQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCTT
 TAAATATGTCAAGATCCAGACTTTTCAGTGTCACTCAGCGATCTCAACGATAGGGATCTTG
 TGTTCGCCGTATTCAGTTGGTGTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
 AAATTATAATGACCAACACCTTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG
 TGGCAGCTCTTCTCTGTGGAGCTGTGGTCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA
 ATTGATTCTCACAGGCGACCATGGCAGTTTTTGGCTGTTGGAGACTTGGACTCTATTTATGG
 GACAGAAGCAGCTGTGAGTCCAACTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT
 ATCCTGTTCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
 AAAACAACCTTGATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA
 AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA
 GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAATTTTGGTCATGGAGATG
 TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC
 AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
 TCCATCATATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC
 CTAGCATGGGGTCCATAAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT
 GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
 GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
 CAGCAAAAACAAGAGGTTTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
 CTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTG
 GCATTTATTGCAGCATCATGCTAAGAACCCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA
 CAAAAACATCCATCAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT
 AAACATCAATAGATATCTAAAAA

FIGURE 228

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSIAISTIGILCLPLFQLVLSLDLPCEEDEMVCVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRTMVFAVGDLDSIYGTEAAVSPTVGIHLQTQTDPDLYP
VPAPCFGPLGSPPPYEEIVKTT
```

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTTGGGACGCAGCTGACGCCCGCTTATTA
 GCTCTCGCTGCGTCGCCCGGCTCAGAAGCTCCGTTGGCGGGCGGCACCGTGACGAGAAGCCC
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACT
 CCTCTTCAAACCTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACTTGGCTGAAG
 ATGAAGAATATACAATATTGAGGATATTTTTTCTTTTTTTTTTCAAGTCTTGATTTGTGGC
 TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTGCTTCTTGAAATGTTTTTTTA
 CAATCTCAAGAAAAATATGTTCCAGAAATGAGTTTACTGTTGCTGTGATTTGGACTCAT
 TGGGGATTGATGTTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAATACTAGACTTAAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAAAAGA
 ACACAGTGGATGTGCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAAAT
 GCTGTCTTCTGGATGACATTTTGCACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
 TGTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA
 CCACAATAAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAAACACCTTGTGC
 TGCTCCATCCACTGTGGATTATATCTTATGGCAGAAAAGCTTTATAATTTGCTGGCTTAGGAC
 AGAGCAATACTTTACAATAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCTATGGAAC
 TCTAATTCTGTACATAAAAAATTTTAAAGTTATTTGTTGCTTTCAGGCAAGTCTGTTCAATG
 CTGTACTATGTCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAAACATGGATTC
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTGGACAAGTGAAGAAATGTTTAA
 TCATTTCTGTCATTTGTTCTCAATAGATGTAAGTCTTTAGACTACGGCTATTTGAAAAATGTG
 CTTATTGTACTATATTTTGTATTCCAAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA
 TAATGTTTTGAAATCATGCCCCAAGAATGTATTGATTTGCATATCTCTCAGATAACTGA
 AGGTTAATTATGTATATTTTAAAAATTACACTTATAAGAGTATAATCTTGAAGTGGGTAG
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAAAATAGTT
 GTAAGCTCTAATCTTATACCTTATTTGAAGAATAAAGATATTTTATGATGAGAGTAACAATA
 AAGTATTCATGATTTTTTACATACATGAATGTTCAATTTTAAAGTTTAACTCTTTGAGTGTCT
 ATGCTATCAGGAAAGCACATTTTCCATATTTGGGTTAATTTTGCTTTTATATATTGGTC
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTTGAGGACTTTAGCCAGGTGTATATAATAA
 GGTACTTTTGTGCTGCATTAAATGCTTGGAAAGTGTAAACATTATATTATATAAGAGTATC
 CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC
 TTAATAAAGAACATTTAAATATAAATATGAAGATTGACTATCTTTTCAGGAAAAAAGCT
 GTATATAGCACAGGGAACCTTAATCTTGGGTAATTTCTAGTATAAAACAAATTTACTTTTAT
 TTAATTTCCCTTGTAGCAATCTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTTATT
 CTCTATAGTAAGTGTCTTAAGTGCAGTCTTCTAGATTAGACTATATAGAATTTAGATAT
 TGTATTGTTCTGTCATTATAATATGCTACCACATGTAGCAATAATACAAATTTTATTAATA
 TAAATATGTGAATATTTGTTTTCATGAAGACAGATTTCCAAATCTCTCTTCTCTCTGTA
 CTGTCTACCTTTATGTGAAGAATTAATTATATGCCATTGCCAGGT

FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR
```

Important features of the protein:**Signal peptide:**

amino acids 1-26

FIGURE 231

CGCGGCCGGGCCCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC
CATGCCCGTGGCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCAGACAAACCCGGCCATGCT
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG
 GTGGATTGTAGCGGCCTGGGCCCCACATCATGCCGTGCCCATCCCTTGGACACAGCCCA
 CTTGGACCTGCTCCAAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGCCGGGCT
 ACACGACGTGGCTGGCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCACCTGCC
 TTCTCCCGCCTTCGCTAGCTGGAGTCGCTTGACCTCAGCCCAATGGCCTGACAGCCCTGCC
 AGCCGAGAGCTTCACCAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACAGCTCCGGG
 AGGTCTCAGTGTCTGCGTTACGACGCACAGTCAGGGCCGGGCACTACACGTGGACCTCTCC
 CACAACCTCATTCACCGCCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCGCCCAACAT
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCCAACCTCCGAGACTTGCCCC
 TGGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCTATTGGTCCGGGTGCCTTCGGGGG
 CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
 TGGCTCCGTGAGCTACCGGGCCTGCAGGTCCTGGACCTGTCGGGCAACCCCAAGCTTAAC
 GGGCAGGAGCTGAGGTGTTTTAGGCTGAGCTCCCTGCAGGAGCTGGACCTTTTCGGGCACC
 AACCTGGTGCCCTGCCTGAGGCGCTGCTCCTCCACCTCCGCGACTGCAGAGGCTGACGCT
 GGGCCAGGATGTGCGGTCGCGCGCCTGGTGGCGGAGGGACCTACCCCCGAGGCTGGCT
 CACGCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCCAC
 ATCTTT**TGA**CAAAATGGTGGCCCCAGGGCCACATAACAGACTGCTGTCTGGGTGCCTCAG
 GTCCCGAGTAACCTTATGTTCAATGTGCCAACACCACTGGGGAGCCGCGAGGCCTATGTGGCA
 GCGTCACCAAGGAGTTGTGGCCCTAGGAGAGGCTTTGGACCTGGGAGCCACCTAGGAGC
 AAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGCACTTCGATGCCA
 AACAGACTCGGGTCCCCCTCCTGCTTCCCTTCCCACTTATCCCCAAAGTGCCCTTCCCTCAT
 GCCTGGGCGGCGCTGACCCGCAATGGGCAGAGGTGGTGGGACCCCTGCTGCAGGGCAGA
 GTTCAGGTCCAATGGGCTGAGTGTCCCTTTGGGCCCATGGCCAGTCACTCAGGGGCGAGTT
 TCTTTTTCAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAGAATCAAGTCCACCTTCTCATGTGAC
 AGATGGGGAAACTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGCC
 ATGACTGGAGCACAGCCTCTGCCTCCAGCCCGGAGCCCAATGCATTTCTTGTCCTCTCTA
 ATAAGCCCCACCCTCCCCGCTGGGCTCCCTTGCTGCCCTTGCCCTGTCTCCCATTAGCACA
 GGAGTAGCAGCAGGACAGGCAAGGAGCCTCACAAGTGGGACTTGGGCGCTCTGACCACT
 GTGCGGCATGGCTTAAGTCACTCTGCCCTTCGGAGCCTTGGAAGCTTAGGGCAGATTGGTT
 CCAGCCTAGCCAGTTTCTCACCCCTGGGTGGGGTCCCCAGCATCCAGACTGGAACCTACC
 CATTTTCCCTGAGCATCTCTAGATGCTGCCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA
 TCTGGCTGGGATCTCCAAGGGCCTCTTGATTAGTCCCACTGGCCCTGAGCACGACAGC
 CCTTCTTACCTTCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCGACCCATGTCTATGC
 TCTACCCCCAGGGCAGCATCTCAGCTTCCGAACCTGGGCTGTTTCTTAGTCTTCACTTTA
 TAAAGTTGTTGCCCTTTTAAACGGAGTGTCACTTTCAACCGGCCTCCCCACCCCTGCTGGC
 CGGGGATGGAGACATGTCACTTTGTAAGAGAGAAAAAGGTTGCATTGTGTCACTTTGTGTAAT
 ATTGTCCTGGGCTGTGTTGGGCTGTTGGGGAGAGCTGGGCATGCTGGCCATGGGCAATC
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTGCTGAC
 CCATCATCTATCTAACCGGTCCTGATTTAATAAACACTATAAAAGGTTTAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLAVSGAQTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESIDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGLTHLSLASLQRLPELAPS
GFRELPGQLVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCGAGTTCCCGTGTGGGTCTGAGG
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATCCCCA
 AAACAAGTTTTGACATTTCCCGTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT
 GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCAC
 GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAAGCCTAAGATGAAAGCC
 TCTAGTCTTGCCCTCAGCCTTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAACCTTCAGGAAATACGAAATG
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
 GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACAGACATTCTTC
 TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAAATATTCGAGGT
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCCACCATCTCTTTACT
 GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGAT
 TGCTTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTGTAAATATCTT
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTGCTATTTAATGTATTT
 ATTTTTTTACTTGGACATGAACTTTAAAAAATTCACAGATTATATTTATAACCTGACTAG
 AGCAGGTGATGTATTTTATACAGTAAAAAATAACCTTGTAATTTCTAGAAGAGTGGCT
 AGGGGGTTATTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
 TATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTGTATGGGAATT
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT
 CTTCAGCCAGGAATCTACAGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA
 CCAAAAAAAAAAAAAAAAAA

FIGURE 234

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNGGATTCATNSHSDSELRP
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISLSANSELTIKKDLRLSHAHMTCHCGEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE

Important features of the protein:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGGCTTTTGCCG
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC
 CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG
 CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
 GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
 TTACAGACACGTAGTGTATTCTGGAGGTCCAATGGTCACATATGAACATCTCCGAGAGGTTG
 TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATG
 GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACCTGACCTAGTGAAGGTTGAGATGCAAAT
 GGAAGGAAAAAGGAACTGGAAGGAAAAACCATTGCGATTTTCGTGGTGATCATGCATTTG
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA
 AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAACACTACTTGGT
 ATTGAATACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
 TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA
 CGAGATAACAAGGAAGGGGACTTTTGATATAAATCATCGACTGACTGCTTGATTTCAGGCTGT
 TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACCATCTTGGCTGAGAATGACCC
 CTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
 TTTTAA

FIGURE 236

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA
RESAPYRGMVRTALGIIEEGFLKLWQGVTPAIYRHHVYSGGRMVITYEHLREVVFVGKSEDEH
YPLWKSIVIGMMAGVIGQFLANPTDLVKVQMMEGKRKLEKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCISGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEFGMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF
```

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGGCGGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
 GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTAAATGAAAAATTTATGC
 TTAAGAAGTAAAAATGCGAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTGCGCAGGTATATTGTTTTTACAGGC
 TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT
 TCACACATGTGGTGTATTTCCACATGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT
 TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTGGTGC
 ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACTTA
 TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC
 TTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTGTAGATAGGTTTTTATCTCTCAGT
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTGTTCCTTACATTTTTATGTTC
 TGAGTTTTGAAATAGTTTTATGAAATTCTTTATTTTTTCATTGCATAGACTGTTAATATGTA
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATCCTGAGATTTAGAA
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT
 CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGG
 CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT
 AAAAAACAAAAATTAGCCAGGCATGGTGGTGGTGCCTGTAATCCCAGCTACCTGGGAGGC
 TGAGGCAGGAGAATCGCTTGAACCCGGGGGCGAGAGTTGCAGTGAGCTGAGTTTGGCCAC
 TGCACTCTAGCCTGGGGGAGAAAGTGAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC
 TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
 TAAAAGGTTTTTCAAGAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTGGTAAAGA
 AAAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCC
 AAAGGACTAGTTTGAAGAGCTTCTTTAAAAAGAATTCTCTAATATGACTTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVVPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFGRTTELWT

Important features:**Signal peptide:**

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
 CTGGCGGGCCCGCAACACTCCGCTCTCACCCCTCTGGGCCCACTGCATCTAGAGGAGGGCCGCTCT
 GTGAGGCCACTACCCTCCAGCAACTGGGAGGTGGGACTGTGAGAAGCTGGCCAGGGTGGT
 GGTACAGTGGGTGAGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAAAGCTGACCCCAAGCCACCCTTCACCTGGACAG
GATGAGAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
 TGTTTATTTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGCTCTGCCACGCTGGCTGGCA
 GCCTCGCCCAACCAAGGAGATCCAGGTTAAAAAGTACAAAGTGTGGCCTCATCAAGCCCTGCCC
 AGCCAACTACTTTGCGTTTAAATCTGCAAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT
 GCTTTGAAGACCGCATGATCATGAGTCTGTGAAAAACAATGTGGGCAGAGGCCTAACATC
 GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCACCTGGTGTGGTGG
 CCTCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAACTCTTCTGTACTTG
 GGGAGTTCTTACGCAAAACAACTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGGTAAAAGCCCCCTTTGAGCAGTTCTTAAAGAACAGCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGGTGGC
 TGTGGCTCTTCTCAGCCAGGGGCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCCG
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCGTGGAAGGTGCTGCAGGTCTTGACGC
 TGTGTGCGCCTCTCCTCTCGGAAACAGAACCCCTCCACAGCACATCTACCCGGAAGACC
 AGCCTCAGAGGGTCTTCTTGAACCAAGCTGTCTGTGGAGAGAATGGGTGCTTTTCGTACGGG
 ACTGCTGACGGCTGTCTGAGGAAGGACAACTGCCAGACTTGAGCCCAATTAAATTTTA
 TTTTGTGCTGTTTGA

FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYSFMSKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCTCTGGGGAT
 CCAGAAACCCATGATACCCTACTGAACACCGAATCCCTGGAAGCCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTCTCTGCTGTCTAGTCTCTAGTCTCAAATTCCCAGTCCC
 CTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTGGATCC
 TGGCTGCAGATGGGGGTCAACACTGGACGTATAGGGGCCCATGGTCAGGACCATTGGCCA
 GCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTGACAGACAGAGTGT
 GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCCGAGC
 CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCATGGGGTCAGAAAGGATC
 CCCAGGGGGGTGAGAACACCAGATCAACAGTGAAGCCACATTTCAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCCTCAGGGCCTGGCT
 GTCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGCAATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCCTCCCTTCAACCTAAGAG
 AGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA
 ACTACCAGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
 CCTTCTCCTGGCTGTTTATTTTCATTGCTAGAAAGATTGGAAGAAGAGGCTGGAAAACCGAA
 AGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCATAAAATTCCTTCTCAGATACCA
 TGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCTCCTTCCCTGGACATCTCTTAGAGAG
 GAATGGACCCAGGCTGTCTATCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTGTTAATGCAGAGANCAAACCTCTGTTTAGTTGCAGGG
 GAAGTTTGGGATATACCCCAAAGTCTCTACCCCTCACTTTTATGGCCCTTTCCTAGATA
 TACTGCGGGATCTCTCTTAGGATAAAGAGTTGCTGTGAAGTTGTATATTTTGTATCAATA
 TATTTGGAAATTAAAGTTTCTGACTTT

FIGURE 242

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812

><subunit 1 of 1, 337 aa, 1 stop

><MW: 37668, pI: 6.27, NX(S/T): 1

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWFPASYPECGNNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHLHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLL
FSTEEEPSKLLVQNYRALQPLNQRMVFASFQAGSSYTTGEMLSLGVGILVGCCLLLAVYF
IARKIRKKRLNRRKSVVFTSAQATTEA

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 243

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTFGTQTHPLTLGGLNVQQQLHPHVLPVFVTQLGAQGTILSSEE
LPQIFTSLSLIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTTPAGRLLTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

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FIGURE 245

GGAGAGAGGCGCGGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCCTCGGAGCGCGGCG
 GAGCCAGACGCTGACCACGTTCTCTCTCCTCGGTCTCCTCCGCTCCAGCTCCGCGCTGCCCG
 GCAGCCGGAGGCC**CATG**CAGCCCCAGGGCCCCGCCCTCCCCGACGCGGCTCCGCGGCCCTCC
 TGCTGCTCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCGGGTACACCTG
 GGATCCCAGGTGCGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAGCTTTGAG
 GAGTCCTGGACACCCAACACAAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT
 TGGGAAAATTGCGGAGGTGACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT
 TCAGTGGCTCACTTCGGCTAAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC
 AATGGAGCTGAATGTTTCAGGACCTCTCCCATTTGAAGCTATAATTTATTTGGACCAAGGAAG
 CCCTGAAATGAATCAACAATTAATATTCATCGCACTTCTCTGTGGAAGGACTTTGTGAAG
 GAATTTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAA
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAA**TA**
AATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGAATGGTTCACTTAAAT
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA
 CCAAAGTGATTTCACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGT
 GGTTCATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA
 TAATTTGGAATATTGTTGTGCTCTTTGTTTTTCTCTTAGTATAGCATTTTTAAAAAATA
 TAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTATATCTGTTAAAT
 AAAAATTATTTCCAACA

FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLIEAIIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217